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OM protein: - protein search, using sw model

Run on: June 2, 2004, 10:44:19 ; Search time 23 Seconds
(without alignments)
558,907 Million cell updates/sec

Title: US-09-807-990-2

Perfect score: 1276

Sequence: 1 MKRVLAVCPAALFSSQALA.....PAFQQQLQKAKAFQHKK 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

1: /cgm2_6/ptodata/2/iaa/5A COMB.psp.*

2: /cgm2_6/ptodata/2/iaa/5B COMB.psp.*

3: /cgm2_6/ptodata/2/iaa/6A COMB.psp.*

4: /cgm2_6/ptodata/2/iaa/6B COMB.psp.*

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6: /cgm2_6/ptodata/2/iaa/backfiles1.psp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1276	100.0	249	3	US-08-750-145A-10
2	1276	100.0	249	3	US-08-975-698A-7
3	1276	100.0	249	3	US-09-417-090-2
4	1276	100.0	249	4	US-09-727-578-8
5	1190	93.3	231	3	US-08-750-145A-10
6	1190	93.3	231	3	US-08-975-698A-7
7	1190	93.3	231	3	US-09-417-090-2
8	1190	93.3	231	3	US-09-727-578-8
9	1158	90.8	248	3	US-08-750-145A-10
10	1158	90.8	248	3	US-08-975-698A-24
11	1158	90.8	248	3	US-09-417-090-24
12	1158	90.8	248	4	US-09-727-578-24
13	1155	90.5	253	4	US-09-489-039A-7933
14	1143	89.6	248	3	US-08-750-145A-22
15	1143	89.6	248	3	US-08-975-698A-26
16	1143	89.6	248	3	US-09-417-090-26
17	1143	89.6	248	4	US-09-727-578-26
18	1014	79.5	249	3	US-08-750-145A-3
19	1014	79.5	249	3	US-08-975-698A-3
20	1014	79.5	249	3	US-09-417-090-3
21	1014	79.5	249	4	US-09-727-578-3
22	1013	79.4	248	3	US-08-750-145A-18
23	1013	79.4	248	3	US-08-975-698A-22
24	1013	79.4	248	3	US-09-417-090-22
25	1013	79.4	248	4	US-09-727-578-22
26	962	75.4	229	3	US-08-750-145A-4
27	962	75.4	229	3	US-08-975-698A-4

28 962 75.4 229 3 US-09-417-090-4
29 962 75.4 229 4 US-09-727-578-4
30 780 61.1 244 3 US-08-750-145A-24
31 780 61.1 244 3 US-08-975-698A-28
32 780 61.1 244 3 US-09-417-090-28
33 780 61.1 244 4 US-09-727-578-28
34 314.5 24.6 252 1 US-07-717-332D-2
35 191 15.0 428 4 US-09-489-039A-10941
36 188.5 14.8 943 4 US-09-540-236-3458
37 175.5 13.8 253 4 US-09-252-991A-28557
38 152 11.9 987 4 US-09-543-681A-7785
39 96 7.5 824 4 US-09-711-164-377
40 90.5 7.1 244 4 US-09-252-991A-21937
41 89.5 7.0 244 4 US-09-543-681A-4595
42 85.5 6.7 187 4 US-09-328-352-7918
43 85.5 6.7 816 4 US-09-540-236-3443
44 84.5 6.6 337 4 US-09-328-352-6980
45 84 6.6 278 3 US-08-961-083-94

ALIGNMENTS

RESULT 1

US-08-750-145A-10

; Sequence 10, Application US/08750145A

; Patent No. 6010851

; GENERAL INFORMATION:

; APPLICANT: MIHARA, Yasuhiro

; APPLICANT: UTAGAWA, Takashi

; APPLICANT: YAMADA, Hideaki

; APPLICANT: ASANO, Yasuhisa

; TITLE OF INVENTION: Method for Producing Nucleoside-5'-

; TITLE OF INVENTION: Phosphate Ester

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.

; STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/750,145A

; FILING DATE: 01-JAN-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 7-149781

; FILING DATE: 05-May-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 8-094680

; FILING DATE: 26-Mar-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: NORMAN F. OBLON

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 249 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:

; ORGANISM: Escherichia blattae

; STRAIN: JCM 1650

US-08-975-698A-10

Query Match 100.0%; Score 1276; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.4e-138;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKRVAVCFPAALFSSQALALVATGN0TTTPDLYLKNSEAINSLALPPPPAVGSIAP 60
DB 1 MKKRVAVCFPAALFSSQALALVATGN0TTTPDLYLKNSEAINSLALPPPPAVGSIAP 60

QY 61 LNDQAMVEQGLLNTERTGKLAARDANLSSGVANAFSGAFSPITEKDAPALHKLITNM 120
DB 61 LNDQAMVEQGLLNTERTGKLAARDANLSSGVANAFSGAFSPITEKDAPALHKLITNM 120

QY 121 IEDAGDLATRSKADHYRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATALVLA 180
DB 121 IEDAGDLATRSKADHYRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATALVLA 180

QY 181 EINFORQNEILKRGYELGQSRVICGYHWCSDVDAARVVGSVAVATLHTNPAPQOOLQKAK 240
DB 181 EINFORQNEILKRGYELGQSRVICGYHWCSDVDAARVVGSVAVATLHTNPAPQOOLQKAK 240

QY 241 AEFQHQKK 249
DB 241 AEFQHQKK 249

RESULT 2

US-08-975-698A-7
; Sequence 7, Application US/08975698A
; Patent No. 6015697
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIRO
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,698A
; FILING DATE: 21-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia blattae
; STRAIN: JCM 1650
US-08-975-698A-7

RESULT 3

US-09-417-090-7
; Sequence 7, Application US/09417090
; Patent No. 6207435
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIRO
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/417,090
; FILING DATE: 13-Oct-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE: 21-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia blattae
; STRAIN: JCM 1650
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-417-090-7

Query Match 100.0%; Score 1276; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.4e-138; Indels 0; Gaps 0;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKVLAVCFPAALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAP 60
DB 1 MKKVLAVCFPAALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAP 60
QY 51 LNDQAMYEQGRLLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAHALHLLTNM 120
DB 61 LNDQAMYEQGRLLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAHALHLLTNM 120
QY 121 IEDAGLATRSADHYMRIRPFYGVSTCNTTEODKLSKNGSYSGHTSIGWATLVLA 180
DB 121 IEDAGLATRSADHYMRIRPFYGVSTCNTTEODKLSKNGSYSGHTSIGWATLVLA 180
QY 181 EINPQRQNEILKRGVELGQSRVICGHHQSDVDAAARVVGSAVVATLHTNPAFQQOLQKAK 240
DB 181 EINPQRQNEILKRGVELGQSRVICGHHQSDVDAAARVVGSAVVATLHTNPAFQQOLQKAK 240
QY 241 AEFAQHOKK 249
DB 241 AEFAQHOKK 249

RESULT 4

US-09-727-578-7
Sequence 7, Application US/09727578
Patent No. 6355472
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0895-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae

STRAIN: JCM 1650
US-09-727-578-7

Query Match 100.0%; Score 1276; DB 4; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.4e-138; Indels 0; Gaps 0;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKVLAVCFPAALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAP 60
DB 1 MKKVLAVCFPAALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAP 60
QY 61 LNDQAMYEQGRLLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAHALHLLTNM 120
DB 61 LNDQAMYEQGRLLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAHALHLLTNM 120
QY 121 IEDAGLATRSADHYMRIRPFYGVSTCNTTEODKLSKNGSYSGHTSIGWATLVLA 180
DB 121 IEDAGLATRSADHYMRIRPFYGVSTCNTTEODKLSKNGSYSGHTSIGWATLVLA 180
QY 181 EINPQRQNEILKRGVELGQSRVICGHHQSDVDAAARVVGSAVVATLHTNPAFQQOLQKAK 240
DB 181 EINPQRQNEILKRGVELGQSRVICGHHQSDVDAAARVVGSAVVATLHTNPAFQQOLQKAK 240
QY 241 AEFAQHOKK 249
DB 241 AEFAQHOKK 249

RESULT 5

US-08-750-145A-11
Sequence 11, Application US/08750145A
Patent No. 6010851
GENERAL INFORMATION:
APPLICANT: MIHARA, Yasuhiro
APPLICANT: UTAGAWA, Takashi
APPLICANT: YAMADA, Hideaki
APPLICANT: ASANO, Yasuhisa
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid

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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia blattae
; STRAIN: JCM 1650
; US-08-975-698A-11
;
Query Match          93.3%  Score 1190; DB 3; Length 231;
Best Local Similarity 100.0%; Pred. No. 1e-128;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 19 LALVATGNDTTTTPDLYLKNSEAINSLALLPPPPAYGSI AFLNDQAMYEQGRLINRTER 78
Db 1 LALVATGNDTTTTPDLYLKNSEAINSLALLPPPPAYGSI AFLNDQAMYEQGRLINRTER 60
;
QY 79 GKLAEDANLSSGGVANAFSGAGSPITEKDAPALHKLNTNMIEDAGDLATRSKAKHYMR 138
Db 61 GKLAEDANLSSGGVANAFSGAGSPITEKDAPALHKLNTNMIEDAGDLATRSKAKHYMR 120
;
QY 139 IRPFAPFVGSTCNTTEODKLSKNGSYPSGHTSIGWATALVLAELNPNQNEILKRGYELG 198
Db 121 IRPFAPFVGSTCNTTEODKLSKNGSYPSGHTSIGWATALVLAELNPNQNEILKRGYELG 180
;
QY 199 QSRVICYGHWQSDVDAARVVGSVAVATLHNPAPFQQQLQKAKAEFAHQKK 249
Db 181 QSRVICYGHWQSDVDAARVVGSVAVATLHNPAPFQQQLQKAKAEFAHQKK 231
;
RESULT 6
US-08-975-698A-8
; Sequence 8, Application US/8975698A
; Patent No. 6015697
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIISA
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,698A
; FILING DATE: 21-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0895-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia blattae
; STRAIN: JCM 1650
; US-08-975-698A-8
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;
; Query Match          93.3%  Score 1190; DB 3; Length 231;
; Best Local Similarity 100.0%; Pred. No. 1e-128;
; Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 19 LALVATGNDTTTTPDLYLKNSEAINSLALLPPPPAYGSI AFLNDQAMYEQGRLINRTER 78
Db 1 LALVATGNDTTTTPDLYLKNSEAINSLALLPPPPAYGSI AFLNDQAMYEQGRLINRTER 60
;
QY 79 GKLAEDANLSSGGVANAFSGAGSPITEKDAPALHKLNTNMIEDAGDLATRSKAKHYMR 138
Db 61 GKLAEDANLSSGGVANAFSGAGSPITEKDAPALHKLNTNMIEDAGDLATRSKAKHYMR 120
;
QY 139 IRPFAPFVGSTCNTTEODKLSKNGSYPSGHTSIGWATALVLAELNPNQNEILKRGYELG 198
Db 121 IRPFAPFVGSTCNTTEODKLSKNGSYPSGHTSIGWATALVLAELNPNQNEILKRGYELG 180
;
QY 199 QSRVICYGHWQSDVDAARVVGSVAVATLHNPAPFQQQLQKAKAEFAHQKK 249
Db 181 QSRVICYGHWQSDVDAARVVGSVAVATLHNPAPFQQQLQKAKAEFAHQKK 231
;
RESULT 7
US-09-417-090-8
; Sequence 8, Application US/09417090
; Patent No. 6207435
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIISA
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/417,090
; FILING DATE: 13-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE: 21-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia blattae
; STRAIN: JCM 1650
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
; US-09-417-090-8
;
Query Match          93.3%  Score 1190; DB 3; Length 231;
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Best Local Similarity 100.0%; Pred. No. 1e-128;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LALVATGNDTTTKPLLYLKNSAINSALLPPPAVGSIAFLNDQAMVEQGRLLNTER 78
Db 1 LALVATGNDTTTKPLLYLKNSAINSALLPPPAVGSIAFLNDQAMVEQGRLLNTER 60

QY 79 GKLAEDANLSSGGVANAFSGAFSPITEKDAFALHKLITNMIEDAGDLATRSKADHYMR 138
Db 61 GKLAEDANLSSGGVANAFSGAFSPITEKDAFALHKLITNMIEDAGDLATRSKADHYMR 120

QY 139 IRPFYFVGVSTNTTEQDKLKNKSGYPSGHTSIGWATLVLAELNFORQNEILKRGYELG 198
Db 121 IRPFYFVGVSTNTTEQDKLKNKSGYPSGHTSIGWATLVLAELNFORQNEILKRGYELG 180

QY 199 QSRVICGVHWSQDVAARVGVSAVVATLTNPAFQOOLQKAKAEFAHQKK 249
Db 181 QSRVICGVHWSQDVAARVGVSAVVATLTNPAFQOOLQKAKAEFAHQKK 231

RESULT 8
US-09-727-578-8
; Sequence 8, Application US/09727578
; Patent No. 6355472
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIKA
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09727,578
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Escherichia blattae
; STRAIN: JCM 1650
US-09-727-578-8

Query Match 93.3%; Score 1190; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 1e-128;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LALVATGNDTTTKPLLYLKNSAINSALLPPPAVGSIAFLNDQAMVEQGRLLNTER 78
Db 1 LALVATGNDTTTKPLLYLKNSAINSALLPPPAVGSIAFLNDQAMVEQGRLLNTER 60

QY 79 GKLAEDANLSSGGVANAFSGAFSPITEKDAFALHKLITNMIEDAGDLATRSKADHYMR 138
Db 61 GKLAEDANLSSGGVANAFSGAFSPITEKDAFALHKLITNMIEDAGDLATRSKADHYMR 120

QY 139 IRPFYFVGVSTNTTEQDKLKNKSGYPSGHTSIGWATLVLAELNFORQNEILKRGYELG 198
Db 121 IRPFYFVGVSTNTTEQDKLKNKSGYPSGHTSIGWATLVLAELNFORQNEILKRGYELG 180

QY 199 QSRVICGVHWSQDVAARVGVSAVVATLTNPAFQOOLQKAKAEFAHQKK 249
Db 181 QSRVICGVHWSQDVAARVGVSAVVATLTNPAFQOOLQKAKAEFAHQKK 231

RESULT 9
US-08-750-145A-20
; Sequence 20, Application US/08750145A
; Patent No. 6010851
; GENERAL INFORMATION:
; APPLICANT: MIHARA, Yasuhiro
; APPLICANT: UTAGAWA, Takashi
; APPLICANT: YAMADA, Hideaki
; APPLICANT: ASANO, Yasuhisa
; TITLE OF INVENTION: Method for Producing Nucleoside-5'-
; TITLE OF INVENTION: Phosphate Ester
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,145A
; FILING DATE: 01-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-149781
; FILING DATE: 05-May-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-094680
; FILING DATE: 26-Mar-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: NORMAN F. OBLON
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Enterobacter aerogenes
; STRAIN: IFO 12010
US-08-750-145A-20

Query Match 90.8%; Score 1158; DB 3; Length 248;
Best Local Similarity 90.3%; Pred. No. 5.5e-125;
Matches 224; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKKRVLAVCAALFSSQALVALVATGNDTTKPDLYLKNSEAINSLALLPPPEVGSIAF 60
Db 1 MKKRVLALCLASFVNAPALVAGNDATTKPDLYLKNQAQIDSLALLPPPEVGSIAF 60
QY 61 INQAMVEQGRLLRNTERGKLAARDANLSSGVANAFSGAFSPITEKDAFALHKLITNM 120
Db 61 INQAMVEKGRLLRNTERGKLAARDANLSSGVANAFSSAFSPITEKDAFQJHKLITNM 120
QY 121 IEDAGLATSAKHVMRIRPFYGVSTCNTTTEQDKLSKNGSVPSGHTSIGWATALVLA 180
Db 121 IEDAGLATSAKEKVMRIRPFYGVSTCNTTTEQDKLSKNGSVPSGHTSIGWATALVLA 180
QY 181 EIPQQRNEILKRGYELGOSRVICGHWQSDVDAARVVGSAVVATLTNPFAFQOOLQKAK 240
Db 181 EIPQQRNEILKRGYELGESRVICGHWQSDVDAARVVGSAVVATLTNPFAFQOOLQKAK 240
QY 241 AFAQHQK 248
Db 241 DEFATQK 248

RESULT 10

US-08-975-698A-24
; Sequence 24, Application US/08975698A
; Patent No. 6315697

GENERAL INFORMATION:

APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIRO

TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/975,698A

FILING DATE: 21-NOV-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 0010-0885-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 248 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Enterobacter aerogenes

STRAIN: IFO 12010

US-08-975-698A-24

Query Match 90.8%; Score 1158; DB 3; Length 248;

Best Local Similarity 90.3%; Pred. No. 5.5e-125;

Matches 224; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKKRVLAVCAALFSSQALVALVATGNDTTKPDLYLKNSEAINSLALLPPPEVGSIAF 60

Db 1 MKKRVLALCLASFVNAPALVAGNDATTKPDLYLKNQAQIDSLALLPPPEVGSIAF 60
QY 61 INQAMVEQGRLLRNTERGKLAARDANLSSGVANAFSGAFSPITEKDAFALHKLITNM 120
Db 61 INQAMVEKGRLLRNTERGKLAARDANLSSGVANAFSSAFSPITEKDAFQJHKLITNM 120
QY 121 IEDAGLATSAKHVMRIRPFYGVSTCNTTTEQDKLSKNGSVPSGHTSIGWATALVLA 180
Db 121 IEDAGLATSAKEKVMRIRPFYGVSTCNTTTEQDKLSKNGSVPSGHTSIGWATALVLA 180
QY 181 EIPQQRNEILKRGYELGOSRVICGHWQSDVDAARVVGSAVVATLTNPFAFQOOLQKAK 240
Db 181 EIPQQRNEILKRGYELGESRVICGHWQSDVDAARVVGSAVVATLTNPFAFQOOLQKAK 240
QY 241 AFAQHQK 248
Db 241 DEFATQK 248

RESULT 11

US-09-417-090-24

; Sequence 24, Application US/09417090
; Patent No. 6207435

GENERAL INFORMATION:

APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIRO

TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/417,090

FILING DATE: 13-Oct-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/975,698

FILING DATE: 21-NOV-1997

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 0010-0885-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 248 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Enterobacter aerogenes

STRAIN: IFO 12010

SEQUENCE DESCRIPTION: SEQ ID NO: 24:

US-09-417-090-24

Query Match 90.8%; Score 1158; DB 3; Length 248;

Best Local Similarity 90.3%; Pred. No. 5.5e-125;

Matches 224; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKKRVLCVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSI AF 60
DB 1 MKKRVLCVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSI AF 60
QY 61 LNDQAMYEQGRLLRNTERRGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 120
DB 61 LNDQAMYEQGRLLRNTERRGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 120
QY 121 IEDAGDLATRSKADHYMRIRPFAPYGVSTCNTTEODKLSKNGSYPSGHTSIGWATALVLA 180
DB 121 IEDAGDLATRSKADHYMRIRPFAPYGVSTCNTTEODKLSKNGSYPSGHTSIGWATALVLA 180
QY 181 EINPQONEILKRGYELGQSRVICGYHWQSDVDAAVVGSVAVVATLHTNPAFOOQLOKAK 240
DB 181 EINPQONEILKRGYELGQSRVICGYHWQSDVDAAVVGSVAVVATLHTNPAFOOQLOKAK 240
QY 241 AEFQHQK 248
DB 241 DEFQHQK 248

RESULT 12

US-09-727-578-24
; Sequence 24, Application US/09727578
; Patent No. 6355472
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIRO
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/727,578
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Enterobacter aerogenes
; STRAIN: IFO 12010
US-09-727-578-24

Query Match 90.8%; Score 1158; DB 4; Length 248;
Best Local Similarity 90.3%; Pred. No. 5.5e-125;
Matches 224; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKKRVLCVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSI AF 60
DB 1 MKKRVLCVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSI AF 60
QY 61 LNDQAMYEQGRLLRNTERRGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 120
DB 61 LNDQAMYEQGRLLRNTERRGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 120
QY 121 IEDAGDLATRSKADHYMRIRPFAPYGVSTCNTTEODKLSKNGSYPSGHTSIGWATALVLA 180
DB 121 IEDAGDLATRSKADHYMRIRPFAPYGVSTCNTTEODKLSKNGSYPSGHTSIGWATALVLA 180
QY 181 EINPQONEILKRGYELGQSRVICGYHWQSDVDAAVVGSVAVVATLHTNPAFOOQLOKAK 240
DB 181 EINPQONEILKRGYELGQSRVICGYHWQSDVDAAVVGSVAVVATLHTNPAFOOQLOKAK 240
QY 241 AEFQHQK 248
DB 241 DEFQHQK 248

RESULT 13

US-09-489-039A-7933
; Sequence 7933, Application US/09489039A
; Patent No. 5610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7933
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7933

Query Match 90.5%; Score 1155; DB 4; Length 253;
Best Local Similarity 89.9%; Pred. No. 1.2e-124;
Matches 223; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 MKKRVLCVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSI AF 60
DB 6 MKKRVLCVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSI AF 65
QY 61 LNDQAMYEQGRLLRNTERRGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 120
DB 66 LNDQAMYEQGRLLRNTERRGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 125
QY 121 IEDAGDLATRSKADHYMRIRPFAPYGVSTCNTTEODKLSKNGSYPSGHTSIGWATALVLA 180
DB 126 IEDAGDLATRSKADHYMRIRPFAPYGVSTCNTTEODKLSKNGSYPSGHTSIGWATALVLA 185
QY 181 EINPQONEILKRGYELGQSRVICGYHWQSDVDAAVVGSVAVVATLHTNPAFOOQLOKAK 240
DB 186 EINPQONEILKRGYELGQSRVICGYHWQSDVDAAVVGSVAVVATLHTNPAFOOQLOKAK 245
QY 241 AEFQHQK 248
DB 246 DEFQHQK 253

RESULT 14

US-08-750-145A-22
; Sequence 22, Application US/08750145A
; Patent No. 6010851
; GENERAL INFORMATION:
; APPLICANT: MIHARA, Yasuhiro

APPLICANT: UTAGAWA, Takashi
APPLICANT: YAMADA, Hideaki
APPLICANT: ASANO, Yasuhisa
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
TITLE OF INVENTION: Phosphate Ester
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-09468C
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: KORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
US-08-750-145A-22

Query Match 89.6%; Score 1143; DB 3; Length 248;
Best Local Similarity 89.1%; Pred. No. 2.9e-123;
Matches 221; Conservative 15; Mismatches 115; Indels 0; Gaps 0;
Qy 1 MKKRVAVCFPAALFSSQALALVATGNDTTTTPDLYLKNSEAINSLALLPPPPVGSIAF 60
Db 1 MKKRVAVCFPAALFSSQALALVATGNDTTTTPDLYLKNSEAINSLALLPPPPVGSIAF 60
Qy 61 LNDQAMTEQGRLLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAHALHKLITNM 120
Db 61 LNDQAMTEQGRLLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAHALHKLITNM 120
Qy 121 IEDAGDLATRSADKHYMRIRPFAYGVSTCNTTTEQDKLSKNGSYPSGHTSIGWATLVIA 180
Db 121 IEDAGDLATRSADKHYMRIRPFAYGVSTCNTTTEQDKLSKNGSYPSGHTSIGWATLVIA 180
Qy 181 EINPQRONEILKRGYELGSGSVICGYHWQSDVDAAIRVGSAAVATLTNPFAQQOQAK 240
Db 181 EINPQRONEILKRGYELGSGSVICGYHWQSDVDAAIRVGSAAVATLTNPFAQQOQAK 240
Qy 241 AEPAQHOK 248
Db 241 DEFACQK 248

RESULT 15

US-08-975-698A-26

Sequence 26, Application US/08975698A
Patent No. 6015697
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIKA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/975,698A
APPLICATION NUMBER: 21-NOV-1997
FILING DATE: 21-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
US-08-975-698A-26

Query Match 89.6%; Score 1143; DB 3; Length 248;
Best Local Similarity 89.1%; Pred. No. 2.9e-123;
Matches 221; Conservative 12; Mismatches 15; Indels 0; Gaps 0;
Qy 1 MKKRVAVCFPAALFSSQALALVATGNDTTTTPDLYLKNSEAINSLALLPPPPVGSIAF 60
Db 1 MKKRVAVCFPAALFSSQALALVATGNDTTTTPDLYLKNSEAINSLALLPPPPVGSIAF 60
Qy 61 LNDQAMTEQGRLLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAHALHKLITNM 120
Db 61 LNDQAMTEQGRLLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAHALHKLITNM 120
Qy 121 IEDAGDLATRSADKHYMRIRPFAYGVSTCNTTTEQDKLSKNGSYPSGHTSIGWATLVIA 180
Db 121 IEDAGDLATRSADKHYMRIRPFAYGVSTCNTTTEQDKLSKNGSYPSGHTSIGWATLVIA 180
Qy 181 EINPQRONEILKRGYELGSGSVICGYHWQSDVDAAIRVGSAAVATLTNPFAQQOQAK 240
Db 181 EINPQRONEILKRGYELGSGSVICGYHWQSDVDAAIRVGSAAVATLTNPFAQQOQAK 240
Qy 241 AEPAQHOK 248
Db 241 DEFACQK 248

Search completed: June 2, 2004, 10:48:05

Job time : 24 secs

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OX protein - protein search, using sw model

Run on: June 2, 2004, 10:47:04 ; Search time 49 Seconds
(without alignments)
1429.660 Million cell updates/sec

Title: US-09-807-990-2

Perfect score: 1276

Sequence: 1 MKKRVLAFCALFFSSQALA.....PAFOOQLQKAKAFQK 249

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/ECT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/ECTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	143	11.2	622	9	US-09-738-626-4817
2	93.5	7.8	353	15	US-10-374-780A-1704
3	97.5	7.6	1610	15	US-10-369-493-3448
4	96.5	7.6	305	15	US-10-369-493-3179
5	96	7.5	178	12	US-10-282-122A-77490
6	96	7.5	824	12	US-10-282-122A-42600
7	95	7.5	824	14	US-10-287-274-377
8	94.5	7.4	515	16	US-10-389-566-351
9	93.5	7.3	704	14	US-10-213-990-21
10	93	7.3	608	15	US-10-369-493-5228
11	92.5	7.2	159	9	US-09-738-626-6679
12	92.5	7.2	159	12	US-10-627-476-102
13	91	7.1	201	14	US-10-156-761-7677
14	90.5	7.1	437	12	US-10-282-122A-66585
15	89	7.0	497	12	US-10-424-599-159028

16	88.5	6.9	168	9	US-09-738-626-6676	Sequence 6676, Ap
17	88	6.9	921	14	US-10-281-866-2	Sequence 2, Appli
18	87	6.8	408	15	US-10-369-493-9754	Sequence 9754, Ap
19	86	6.7	273	12	US-10-435-114-63365	Sequence 63365, A
20	86	6.7	665	12	US-10-282-122A-51723	Sequence 51723, A
21	86	6.7	1573	14	US-10-214-766-35	Sequence 35, Appl
22	85.5	6.7	221	12	US-10-282-122A-69103	Sequence 69103, A
23	85.5	6.7	774	12	US-10-282-122A-63166	Sequence 63166, A
24	85	6.7	766	14	US-10-317-832-120	Sequence 120, App
25	84.5	6.6	4317	12	US-10-282-122A-67862	Sequence 67862, A
26	84	6.6	278	9	US-09-765-272-94	Sequence 94, Appli
27	84	6.6	571	9	US-09-765-272-4	Sequence 4, Appli
28	84	6.6	981	14	US-10-156-761-15071	Sequence 15071, A
29	83.5	6.5	260	16	US-10-408-765A-1756	Sequence 1756, Ap
30	83	6.5	268	12	US-10-282-122A-63138	Sequence 63138, A
31	83	6.5	378	15	US-10-369-493-5080	Sequence 5080, Ap
32	83	6.5	535	14	US-10-032-201B-232	Sequence 232, App
33	82.5	6.5	402	14	US-10-081-051-16	Sequence 16, Appl
34	82	6.4	610	12	US-10-282-122A-45687	Sequence 45687, A
35	81.5	6.4	198	12	US-10-282-122A-50258	Sequence 50258, A
36	81.5	6.4	265	12	US-10-424-599-243256	Sequence 243256, A
37	81.5	6.4	349	15	US-10-150-048-4	Sequence 4, Appli
38	81.5	6.4	518	9	US-09-738-626-4323	Sequence 4323, Ap
39	81.5	6.4	928	15	US-10-379-632-33	Sequence 93, Appl
40	81.5	6.4	1063	15	US-10-379-632-84	Sequence 84, Appl
41	81.5	6.4	1089	15	US-10-379-632-109	Sequence 103, App
42	81.5	6.4	1113	15	US-10-379-632-103	Sequence 103, App
43	81.5	6.4	1209	15	US-10-379-632-96	Sequence 96, Appl
44	81	6.3	298	12	US-10-282-122A-47486	Sequence 47486, A
45	81	6.3	490	15	US-10-369-493-2735	Sequence 2735, Ap

ALIGNMENTS

RESULT 1

US-09-738-626-4817
; Sequence 4817, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patent in ver. 3.0
; SEQ ID NO 4817
; LENGTH: 622
; TYPES: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4817

Query Match 11.2%; Score 143; DB 9; Length 622;
Best Local Similarity 27.4%; Pred. No. 3.3e-06;
Matches 49; Conservative 24; Mismatches 72; Indels 34; Gaps 6;

Qy 83 AEDANLSSGGVANA----FSGAFGSPITEKADPAHLKLLTNMIEDAGLATRSADHYMR 138

Db 159 ATTATKNDGNGVNGWAETGELGSLTVDLIEAIPQHAATSN-----NAKAYQY 207
QY 139 IRFPAP-----YGVST--CNTTEQD--KLSKNGSYSPSGHTSIGWATALLVLAETIN 183
Db 208 PRFYRWTESIEPEAWGSGVDMPEYANPLRKDESEASADGGPPSGHTSAGGMAITGLAYAF 267
QY 184 EQCNEILKRGVYELGQSGSVICGVHMQSDVDAARVVGSAVVATLHTNPAFCQOQLOKAKAE 242
Db 268 PQYDKLLMTAAEIGESRIQLGMSPLDVGGRVLSTAITAGALNDP-----NLSVRAE 322

RESULT 2

US-10-374-780A-1704
; Sequence 1704, Application US/10374780A
; Publication No. US20040019927A1

GENERAL INFORMATION:

; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Keddle, James
; APPLICANT: Brown, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS

; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A

; CURRENT FILING DATE: 2003-02-25

; PRIOR APPLICATION NUMBER: 09/837,944

; PRIOR FILING DATE: 2001-04-18

; PRIOR APPLICATION NUMBER: 60/310,847

; PRIOR FILING DATE: 2001-08-09

; PRIOR APPLICATION NUMBER: 09/934,455

; PRIOR FILING DATE: 2001-08-22

; PRIOR APPLICATION NUMBER: 60/336,049

; PRIOR FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/338,692

; PRIOR FILING DATE: 2001-12-11

; PRIOR APPLICATION NUMBER: 10/171,468

; PRIOR FILING DATE: 2002-06-14

; PRIOR APPLICATION NUMBER: 10/225,066

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: 10/225,067

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: 10/225,068

; PRIOR FILING DATE: 2002-08-09

; NUMBER OF SEQ ID NOS: 2906

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1704

; LENGTH: 353

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Orthologous to G1652

US-10-374-780A-1704

Query Match 7.8%; Score 99.5; DB 15; Length 353;

Best Local Similarity 24.5%; Pred. No. 0.077; 92; Indels 71; Gaps 13;

Matches 63; Conservative 31; Mismatches 92; Indels 71; Gaps 13;

QY 41 EAINSLALLP--PPPVGSIATLNDQAMYEQRLRN---TERGKLAED-----AN 87

Db 13 ETLQHILPLATPPPPAGGYA--GENATFPQLALRESSVQNGNAPPEPTAHECHRASN 70

QY 88 LSSGGVANAFSGATGSPITEKDA-----PALHKLITNMIED 123

Db 71 SWSGSDTDSVSGGGGAGVMEHDGHTSPNSVRCAGGGGGGGGGLWVPSNFFSSAMTQP 130
QY 124 AGDIATSAKDHVMRIRPFAPYG-----YSTNTTTEQDKLSK--NSGYSFGHTSI 171
Db 131 CNDQATPSNPPTTTTRAR-----YGGGVRYLPAAVSPSPSAQTRRASSKXGNGGGSGSSA 186
QY 172 G-WATALVLAEINPQRCNEILKRGVYELGQSGSVICGVHMQSDVDAARVVGSAVVATLHTNP 230
Db 187 APYACEHIIAE--RRREKINQRFIEL--SVIPEL---KXMDKATILSDAV----- 231
QY 231 AFQOQLOKAKAEFAHQ 247
Db 232 RYVKEMQEKLEHQ 248

RESULT 3

US-10-369-493-3448

; Sequence 3448, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 3448

; LENGTH: 1610

; TYPE: PRT

; ORGANISM: Neurospora crassa

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(1610)

; OTHER INFORMATION: unsure at all xaa locations

US-10-369-493-3448

Query Match 7.6%; Score 97.5; DB 15; Length 1610;

Best Local Similarity 26.4%; Pred. No. 1.3;

Matches 53; Conservative 21; Mismatches 70; Indels 57; Gaps 10;

QY 18 ALALVAT-GNDTTTKPDILYLNKSE-----AINSLALLPPPPAV-----GSIA-FL 61

Db 274 ALPLGATMGNDMTNGNLDEAHGSEQHPPPPFASVNVDPDPFGVIYEDPTAEACGKIQFEL 333

QY 62 ND-----QAMVEQGRLLRNTERKLAEDANLSSGGVANAFSGAFSGPITEKDA---PA 112

Db 334 NNLTTTLQNTWKOLRDMLETHQW-----FASHVEERAKAQPN 374

QY 113 LHKL---LITNMIEDAGDIATSAKDHVMRIRPFAPYGVSTCTMTTEQDKLSKNGSYSPSGHT 169

Db 375 YHOVYLD-VKMFEDK-SLWAEVLRETVSVQRMENLSDVTLQNSTERTHLKNLG----- 426

QY 170 SIGNATALVLAEINPQRCNEI 190

Db 427 --GWLGLTLARNKPIKRN 445

RESULT 4

US-10-369-493-3179

; Sequence 3179, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xiaofeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-13(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3179
LENGTH: 305
TYPE: PRT
ORGANISM: Neurospora crassa
US-10-369-493-3179

Query Match 7.6%; Score 96.5; DB 15; Length 305;
Best Local Similarity 22.2%; Pred. No. 0.13;
Matches 43; Conservative 29; Mismatches 79; Indels 43; Gaps 7;
QY 3 KRVLCVCAALFSSQALVALVATGNDTTTKEDLYLKNSEA:INSLALLPPPPAVGSIAPLN 62
DB 84 KRSIDACLADJ-----DGHK-DIP-----EPARIDPKVPLESTLXLE 122
QY 63 DQ-----AMYEQRLNTERGKLAEDANLS-----SGGVANAFSGAPGS 103
DB 123 DEVYSGIIGIGLSEVSAATIRKAVKITKIAAVEVEISLWATHLENGVAEA-CAEFGI 181
QY 104 PTEKAPALHKLITNMIEDAGLATSADKHMYRIRPFYFVSTCNTTEQDKLSKNGS 163
DB 182 FLIAY-SPISQGLTGQIKTLDLADDFRRHPRFPENFH-LNIQLVSELNLAKKG 239
QY 164 YPSGHTSIGWATAL 177
DB 240 YTPAQLAINVKS 253

RESULT 5
US-10-282-122A-77490
Sequence 77490, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 42600
LENGTH: 824

PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 77490
LENGTH: 178
TYPE: PRT
ORGANISM: Vibrio cholerae
US-10-282-122A-77490

Query Match 7.5%; Score 96; DB 12; Length 178;
Best Local Similarity 31.0%; Pred. No. 0.066;
Matches 27; Conservative 14; Mismatches 42; Indels 4; Gaps 1;
QY 133 KDHMYRIRPFYFVSTCNTTEQDKLSKNGYPSGHTSIGWATALVLAIEINPORQNEILK 192
DB 81 KNSPQRRPQELSALVTAYITPSDRY----SLPSGHTAAAFVMTLIGYIYPHWYAVALC 136
QY 193 RGYELGQSRVICGVHWSQDVAARVVG 219
DB 137 WAGLIGLARVLLGVHLSDDVTAGALLG 163

RESULT 6
US-10-282-122A-42600
Sequence 42600, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 42600
LENGTH: 824


```
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-21

Query Match      7.3%; Score 93.5; DB 14; Length 704;
Best Local Similarity 21.3%; Pred. No. 0.99;
Matches 53; Conservative 44; Mismatches 67; Indels 85; Gaps 14;

Qy 22 VATGNDTTTKEDLYLKNSEALNSLALPPPPAVGSI AFLNDQAMVEQGRLLNTERGK- 80
Db 151 ILLASPSQSNEDYYITWTRDAALTKYL-----VGSFAADHDPALQ---RIIEDYVESQA 202

Qy 81 ----LAEDANLSSGV-----ANAFSGAFGSPITEKDPALHK-----LTNMIEDA 124
Db 203 HLQIVSPNSGNLSSGGLPEKLRVDSGSAFHSWGEP--QSDGPALGATLLISYANLMDN 260

Qy 125 GDLATRAKDHMYRIRP-----AFYGVSTCTNTEQDKLSKNGSPSGHTSIGHAT 175
Db 261 GYFSTVESS-----IWPLIQNDLSYLTEFWNSSTFDLME-----VGSSEF-----FTT 304

Qy 176 ALVLAEINPQRNEILKRGYELGO-----SRVIC--GYHWQSDVDAAARVVG 220
Db 305 AV-----QHQAALRGAALQRLGKTCNQCQSAFQVLCFLQTY-----TGS 346

Qy 221 AVVATLHTN 229
Db 347 SILANLYSD 355

RESULT 10
US-10-369-493-5228
; Sequence 5228, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiaofeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5228
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5228

Query Match      7.3%; Score 93; DB 15; Length 608;
Best Local Similarity 23.5%; Pred. No. 0.9;
Matches 42; Conservative 19; Mismatches 78; Indels 40; Gaps 5;

Qy 84 EDANLSSGAVANAFSGFSGP-TEKDPALHKLNTNMIEDAGDLATRAKDHMYRIRPPA 143
Db 456 EDGQAFGGGGNGMNAFGMDV-ENDDPLALALRVSMEEERARQAAAAAN-----505

Qy 144 FYGVSTCTNTEQDKLSKNGSPSGHTSIG-----WATLVLAELNIPQRNEILKRG 194
Db 506 --GGAADSGADAEVAAAAAAPLEMDNGAMTEEQLEWALRLSMQENAPAFQPVQV----559

Qy 195 YELQSRVICGYHWQSDVDAAARVVGSAVVATHTNPAFQQ-----LQAKAEFAHQKK 249
Db 560 -----CHEQMDVGGAPAVGDNLDLCANNPELLQIVVDLPAANAEKKDDQKK 607

RESULT 11
US-09-738-626-6679
; Sequence 6679, Application US/09738626
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```
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patent in ver. 3.0
; SEQ ID NO 6679
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6679

Query Match      7.2%; Score 92.5; DB 9; Length 159;
Best Local Similarity 24.2%; Pred. No. 0.13;
Matches 40; Conservative 26; Mismatches 54; Indels 45; Gaps 8;

Qy 93 VANAFSG---AFGSP-----TEKDPAL---HKLNTNMIEDA-----GDLATESAK 133
Db 5 ILDAFGLRVTWLSPVILFTQTGLTFVVALVWGLRKATAPIAVLGLANLISHFLK 64

Qy 134 DHYMRIRPFYGVSTCTNTEQDKLSKNGSPSGHTSIGWATLVLAELNIPQRNEILK 193
Db 55 RAPEPRP-----NTAEHLVVTETNFSFSGH-AVGAACAVAVGVS-----VNR 107

Qy 194 GYEL-----GQSRVICGYHWQSDVDAAARVVGSAVVATHTN 229
Db 108 WWKLTALVIALVGLSRLVGVGVHWPSPDVLGAWAIGALTSVVVFTS 152

RESULT 12
US-10-627-476-102
; Sequence 102, Application US/10627476
; Publication No. US20040030116A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schoder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CPCN
; CURRENT APPLICATION NUMBER: US/10/627,476
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 09/602,787
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
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; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 102
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-627-476-102

Query Match      7.1%; Score 92.5; DB 12; Length 159;
Best Local Similarity 24.2%; Pred. No. 0.13;
Matches 40; Conservative 26; Mismatches 54; Indels 45; Gaps 8;

Qy 93 VANAFSG---AFGSP---TEKDAPL---HKLTTNIEDA-----GLATRSK 133
Db 5 ILDAFGLRVTWLSPILETLTGPTLMFVYALVWGLRKSATAPAVGLAMLISHFLK 64
Qy 134 DYMWRPFAFYGVSTCTNTEQDKLXNGSVPSGHTSIGWATALVLAELINPQNEILKR 193
Db 65 RAPERPRP-----NTAEHLVWTFNFPFSGH-AVGAACAVAVGYS-----VNR 107
Qy 194 GYEL-----GQSRVICYGHMQSDVDAARVVGSVAWATLHN 229
Db 108 WKKLTWLVIALVGLSLRYGVHVPDVLGAWGALGTSVVWF'S 152

RESULT 13
US-10-156-761-7677
; Sequence 7677, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, HIROSHI
; APPLICANT: HORIKAWA, JUN
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, YASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 245-262
; CURRENT APPLICATION NUMBER: US/10/156.761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 7677
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-7677

Query Match      7.1%; Score 91; DB 14; Length 201;
Best Local Similarity 30.3%; Pred. No. 0.28;
Matches 33; Conservative 11; Mismatches 45; Indels 20; Gaps 3;

Qy 142 FAFYGS-----TCN-----TTEQDKLXNGSVPSGHTSIGWATALVLAELINPQ 185
Db 74 FAAYGVNDVLKLVREDRPPCQSLQVITLACPAFGDWSFPNSNHTAIAAAMALLFVSR 133
Qy 186 RQNEILKRGYELGOSRVICGVHMQSDVDAARVVGSVAVA-----THTNP 230
Db 134 LGVAAGACAMAASRVVWGAHPDVAAGVVGVGVAALAMVTLRRQP 182
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RESULT 14
US-10-282-122A-66585
; Sequence 66585, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78514
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66585
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66585

Query Match      7.1%; Score 90.5; DB 12; Length 437;
Best Local Similarity 26.4%; Pred. No. 1;
Matches 34; Conservative 24; Mismatches 48; Indels 23; Gaps 5;

Qy 105 ITEKDAPALMKLLTNMIEDAGDLATRSKAKOHYMRIRPFAYGVSTCTNTEQDKLXNGSY 164
Db 274 LTRQWRPAIFAGT-LVGTA--LANQTLKTLFARARPEVL-----AEPLS-SFSP 319
Qy 165 PSHTSIGWATALVLAELINPQNEILKRGY-----ELGOSRVICGVHMQSDVDA 215
Db 320 PSCHSSASFAFFLTGLVIASRQPPRWRLTWLLAVIPSLIALSRVYLVGHVWPSDIVAG 379
Qy 216 RVGSAVVA 224
Db 380 ALLATTVC 388

RESULT 15
US-10-424-599-159028
; Sequence 159028, Application US/10424599
; Publication No. US20040031072A1
```

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; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 159028
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_114622C.1.pep
US-10-424-599-159028

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Query Match      7.0%; Score 89; DB 12; Length 497;
Best Local Similarity 24.2%; Pred. No. 1.8;
Matches 52; Conservative 35; Mismatches 84; Indels 44; Gaps 10;

Qy      6 LAVCFALFSSQALALVATGNDTTTKPDLYYLKNSEAINSLALPPPPAVGSIATINDQA 65
Db      301 LCVSFAGIYNSDPVLAV---KYLKEEPTAETAEVAVTGEKL-----TSPLNNNA 348

Qy      56 MYEQGRLLRNTERGKLAEDANL-SSGGVANAFSGAFGSPITEKDAPALHKLITNNIEDA 124
Db      349 AYLE--VLKVAQYKLHQAARHVSSEAKRVHAFKDVVSSNLSDE-----MLKKL 396

Qy      125 GDLATRGAQKHMYRIRPEAFYGVSTCNTTEQDKL-----SKNGSYPSGHTSICW---ATAL 177
Db      397 GDLMNES--HSCSV-----LYECSCELEELVNICNNGALGARLTGAGWGSCAVAL 447

Qy      178 VLAENPCQRNEILKRGYELGQSRVICGYHQCJV 212
Db      448 VKESIVPQFIILNKECFY---QSRIDKGVKKNDL 479

```

Search completed: June 2, 2004, 10:52:58
Job time : 50 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2004, 10:43:19 ; Search time 20 Seconds
(without alignments)
1197.584 Million cell updates/sec

Title: US-09-807-990-2

Perfect score: 1276

Sequence: 1 MKKRVLAVCFALFSSQALA.....PAFQQQLQKAKFAHQKX 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1014	79.5	249	1 S19187	acid phosphatase (
2	1013	79.4	248	1 PAOFCS	acid phosphatase (
3	486	38.1	250	1 A41330	acid phosphatase (
4	477	37.4	250	2 A51025	acid phosphatase (
5	339.5	26.6	264	1 A32044	acid phosphatase (
6	274.5	21.5	258	2 E87293	acid phosphatase (
7	189.5	14.9	2314	2 T28638	hypothetical prote
8	175.5	13.8	241	2 C83621	probable acid phos
9	167	13.1	591	2 C96991	uncharacterized pr
10	141	11.1	660	2 A31118	serine proteinase
11	141	11.1	660	2 E38169	serine proteinase
12	105	8.2	145	2 F75447	vanadium chloroper
13	99.5	7.8	259	2 A37623	PAP2 homolog prote
14	96.5	7.6	256	2 G39845	dihydroxylate deh
15	96	7.5	178	2 D82070	conserved hypothet
16	96	7.5	824	2 D64738	ATP-dependent heli
17	95	7.4	320	2 A32020	hypothetical prote
18	94	7.4	824	2 H85498	helicase, ATP-depe
19	94	7.4	824	2 H90647	ATP-dependent heli
20	93	7.3	608	2 D87912	protein B0205.3 [i
21	91	7.1	217	2 D97672	hypothetical prote
22	91	7.1	242	2 A32897	conserved hypothet
23	90.5	7.1	437	2 H31143	hypothetical prote
24	89.5	7.0	1157	2 A35152	PAS1 protein - yea
25	88	6.9	589	2 T29897	hypothetical prote
26	86.5	6.8	368	2 A32148	probable porin vc1
27	86.5	6.8	649	2 S74823	N-acetylmuramoyl-L
28	86	6.7	292	2 A33647	phosphatidyglycer
29	86	6.7	665	2 F97032	beta-glucosidase i

ALIGNMENTS

RESULT 1

S19187
acid phosphatase (EC 3.1.3.2) - Morganella morganii
C:Species: Morganella morganii
C:Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 18-Aug-2003
C:Accession: S19187
R:Thaller, M.C.; Berlutti, F.; Schippa, S.; Roessolini, G.M.
submitted to the EMBL Data Library, February 1992
A:Description: Sequencing the Morganella morganii phoC gene coding for a periplasmic ac
A:Reference number: S19187
A:Accession: S19187
A:Molecule type: DNA
A:Residues: 1-249 <THA>
A:Cross-references: EMBL:X64444; NID:G44463; PIDN:C445774.1; PID:G44464
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
C:Keywords: phosphoric monoester hydrolase
F:109-222/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match 79.5%; Score 1014; DB 1; Length 249;
Best Local Similarity 77.1%; Pred. No. 2.5e-81;
Matches 192; Conservative 23; Mismatches 34; Indels 0; Gaps 0;

QY	1	MKKRVLAVCFALFSSQALALVATNDTTKEDLYLKNSEAINSLALPPEAVGSIAF	60
DB	1	MKKRIIACGLFSLFSLALAAIPAGNDATTKEDLYLKNQQAIDSLKLEPPEVGSIOF	60
QY	61	LNQDMYEQGRLLRNTERGKLAEDANLSSGGVANAFSGAFGSPITEKDAFALHKLITNM	120
DB	61	LNQDMYEGKMLRNTERGKQAQADADLAAGVATAFSGAFGYPITEKDSPELYKLLTNM	120
QY	121	IEDAGDLATRSADKHYMRIRPFYGVSTONTTEQDKLSKNGSYSGHTSIGWATLVLA	180
DB	121	IEDAGDLATRSADKHYMRIRPFYGTETCNTKQCKLSTNGSYSGHTSIGWATLVLA	180
QY	181	EINPORQNEILKRGVEIQSGVICGHWQSDVDAARVGVSAVATLHTNPAAQQLQKAK	240
DB	181	EVPANQDAIILERGVLQGSQVIGCQHWQSDVDAARIIVGSAVATLHSDPAFQAQAKAK	240
QY	241	AEFAQHOKX	249
DB	241	QEFAKSKX	249

RESULT 2

PAOFCS
acid phosphatase (EC 3.1.3.2) - Providencia stuartii
C:Species: Providencia stuartii
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Aug-2003
C:Accession: S19888
R:Riccio, M.L.; Lombardi, G.; Chiesurin, A.; Satta, G.
submitted to the EMBL Data Library, February 1992
A:Reference number: S19888

A:Accession: S19888
A:Molecule type: DNA
A:Residues: 1-248 <RIC>
A:Cross-references: EMBL:X64820; NID:G45861; PIDN:CAA46032.1; PID:G45862
C:Genetics:
A:Gene: phoN
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
C:Keywords: phosphoric monoester hydrolase
F:109-222/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match 79.4%; Score 1013; DB 1; Length 248;
Best Local Similarity 77.4%; Pred. No. 3e-81;
Matches 192; Conservative 26; Mismatches 30; Indels 0; Gaps 0;

QY 1 MKKRVAVCFALFSSQALALVATGNTTTKPDLYLKNSEAFNSLALLPPPPAVGSI 60
DB 1 MKKLLAVFCAGAFVSTVFAPFAGNDVTTKPDLYLKNSEAFNSLALLPPPPAVGSI 60

QY 61 LNDQAMVEQGRLLRNTERRGKLAEDANLSSGCVANAFSGAFSPITEKDAPEIHKLLTNM 120
DB 61 LNDQAMVEQGRLLRNTERRGKLAEDANLSSGCVANAFSGAFSPITEKDAPEIHKLLTNM 120

QY 121 IEDAGLATRSKADHYNRIRPPAFYGVSTCNTTTEQDKLSKNGSYPSGHTSIGWATLVLA 180
DB 121 IEDAGLATRSKADHYNRIRPPAFYGVSTCNTTTEQDKLSKNGSYPSGHTSIGWATLVLA 180

QY 181 EIPNPOQNEILKRGYELGQSRVIGYHWSQVDAARVVGSAVATLTNPAFQOOLQAK 240
DB 181 EIPNPOQNEILKRGYELGQSRVIGYHWSQVDAARVVGSAVATLTNPAFQOOLQAK 240

QY 241 AEPAQOK 248
DB 241 DEFAKUK 248

RESULT 3
A41330
acid phosphatase (EC 3.1.3.2) PhoN precursor - Salmonella typhimurium
N:Alternate names: glycerophosphatase; nonspecific acid phosphatase; phosphomonoesterase
C:Species: Salmonella typhimurium
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Aug-2003
C:Accession: S20958; A41330; S14515; S18926
R:Grisman, E.A.; Sailer Jr., M.H.; Ochman, H.
EMBO J. 11, 1309-1316, 1992
A:Title: Horizontal transfer of a phosphatase gene as evidence for mosaic structure of t
A:Reference number: S20958; MUID:92224869; PMID:1139343
A:Accession: S20958
A:Molecule type: DNA
A:Residues: 1-250 <GRO>
A:Cross-references: EMBL:X63599; NID:G47823; PIDN:CAA45144.1; PID:G47824
R:Kasahara, M.; Nakata, A.; Shinagawa, H.
J. Bacteriol. 173, 6760-6765, 1991
A:Title: Molecular analysis of the Salmonella typhimurium phoN gene, which encodes nonse
A:Reference number: A41330; MUID:92041557; PMID:1938882
A:Accession: A41330
A:Molecule type: DNA
A:Residues: 1-229, 'SVRS' <KAS>
A:Cross-references: GB:X59036; NID:G48894; PIDN:CAA41760.1; PID:G48895
C:Genetics:
A:Gene: phoN
A:Map position: 96 min
A:Note: regulated by the two-component regulatory system consisting of phoP and phoQ
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic do
C:Keywords: periplasmic space; phosphoric monoester hydrolase
F:108-221/Domain: glucose-6-phosphatase catalytic domain homology <GPH>

Query Match 38.1%; Score 486; DB 1; Length 250;
Best Local Similarity 43.0%; Pred. No. 4.6e-35;
Matches 104; Conservative 33; Mismatches 95; Indels 10; Gaps 2;

QY 1 MKKRVAVCFALFSSQALALVATGNTTTKPDLYLKNSEAFNSLALLPPPPAVGSI 60
DB 1 MKSRYLVFFLLIVAKYTS-----ETVQF---FHSPEESVNSQFYLPPEPPGNDPPAY 50

QY 61 LNDQAMVEQGRLLRNTERRGKLAEDANLSSGCVANAFSGAFSPITEKDAPEIHKLLTNM 120
DB 51 RYDKAEYFKYAIKSGPRWKAEDADVSVENIARIFSPVVGAKINFDPEETWNMLKYL 110

QY 121 IEDAGLATRSKADHYNRIRPPAFYGVSTCNTTTEQDKLSKNGSYPSGHTSIGWATLVLA 183
DB 111 LTMGGYVATASAKKYMRTPFPVLEHNHSTCRPEDNLTNRKNGSYPSGHTSIGWATLVLA 170

QY 181 EIPNPOQNEILKRGYELGQSRVIGYHWSQVDAARVVGSAVATLTNPAFQOOLQAK 240
DB 171 EAPPERAQELARRGEGQSRVIGCAHWQSDVDAGRYVGAVEFARLQTIPIAFQSLAKVR 230

QY 241 AE 242
DB 231 EE 232

RESULT 4
AF1025
acid phosphatase (EC 3.1.3.2) - Salmonella enterica subsp. enterica serovar Typhi (stra
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 25-Aug-2003
C:Accession: AF1025
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AF1025
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250 <PAR>
A:Cross-references: GB:ALU513382; PIDN:CAD09303.1; PID:G16505305; GSPDB:GN00176
C:Genetics:
A:Gene: phoN
C:Superfamily: nonspecific acid phosphatase, class A; glucose-6-phosphatase catalytic d
C:Keywords: phosphoric monoester hydrolase

Query Match 37.4%; Score 477; DB 2; Length 250;
Best Local Similarity 47.3%; Pred. No. 2.9e-34;
Matches 95; Conservative 31; Mismatches 75; Indels 0; Gaps 0;

QY 41 EAINSLALLPPPPAVGSIATLNDQAMTEQGRLLRNTERRGKLAEDANLSSGCVANAFSGA 100
DB 31 ESVNSQYVLPDPGNDPPAFRYDKAEAFKGYAIKSGPRWKAEDADVSVENIARIFSPV 90

QY 101 FGSPITEKDAPEIHKLLTNMIEDAGLATRSKADHYNRIRPPAFYGVSTCNTTTEQDKLSK 160
DB 91 VGAKINFDPEETWNMLKYLKMGYYATASAKKYMRTPFPVLEHNHSTCRPEDNLTNRK 150

QY 161 NGSYPSGHTSIGWATLVLAIEINPQRQNEILKRGYELGQSRVIGYHWSQVDAARVVG 220
DB 151 DGSYPSGHTSIGWATLVLAIEINPQRQNEILKRGYELGQSRVIGYHWSQVDAARVVG 210

QY 221 AVVATLTNPAFQOOLQAKAE 242
DB 211 VEFARLQTIPIAFQSLAKVR 232

RESULT 5
A32044
acid phosphatase (EC 3.1.3.2) - Zymomonas mobilis
C:Species: Zymomonas mobilis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Aug-2003
C:Accession: A32044
R:Pond, J.L.; Eddy, C.K.; Mackenzie, K.F.; Conway, T.; Borecky, D.J.; Ingram, L.O.
J. Bacteriol. 171, 767-774, 1989
A:Title: Cloning, sequencing, and characterization of the principal acid phosphatase, t
A:Reference number: A32044; MUID:89123152; PMID:23914872

Query Match 8.2%; Score 105; DB 2; Length 145;
Best Local Similarity 37.5%; Pred. No. 0.055;
Matches 24; Conservative 9; Mismatches 31; Indels 0; Gaps 0;

QY 163 SYPSGHTSICGATVLAELNPNQNEILKRGYELGQSRVFCGHWGSDVDAARVGSV 222
DB 77 SYPSGHTVSGAAEVLQFFPLQARQLRDARDAFVRVGGIHWGVDGVLGVGRV 136

QY 223 VATEL 226
DB 137 ARAL 140

RESULT 13
A87623
PAP2 homolog protein [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 02-Jun-2003
R:Accession: A87623
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, V.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
D.; J.; Zmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: A87623
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-259 <STO>
A:Cross-references: GB:AF005673; NID:gl3424659; PIDN:AAK24981.1; GSPDB:GN0C148
C:Genetics:
A:Gene: CC3019
C:Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain hom

Query Match 7.8%; Score 99.5; DB 2; Length 259;
Best Local Similarity 28.0%; Pred. No. 0.36;
Matches 47; Conservative 15; Mismatches 63; Indels 43; Gaps 5;

QY 88 LSSGVANAFSGAFSGSPITEKDPALHK-LLTNNIEDA----- 124
DB 76 LRVGGQNALVGPDLHVAVDITLGSVAVLTLLIARFALLGSLKRWTEAWLLALGAL 135

QY 125 -GDLATRSADKHMYRIRPFYFGVSTCNTTQDKLSKNGSPSGHTSIGWATLVL----- 179
DB 136 SGVTVSGLKAVFGRERPDYRVVE-----AVNASPFGHMLSAVVFLTLGVLA 186

QY 180 AEINPORONEILKRGYE-----LQSRVLCGYHWQSDVDAARVGS 221
DB 187 ARFSERRVKILAVSAAVVSVLLVGSRVYLGHWVSDVLGWSVGAA 234

RESULT 14
G39845
dihydroorotate dehydrogenase (electron transfer subunit) pyrdII - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 20-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 21-Jul-2000
A:Accession: G39845; D69686
R:Quinn, C.L.; Stephenson, B.T.; Switzer, R.L.
J. Biol. Chem. 265, 9113-9127, 1991
A:Title: Functional organization and nucleotide sequence of the Bacillus subtilis pyrim
A:Reference number: A39845; MUID:91225016; PMID:1709162
A:Accession: G39845
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-256 <OUT>
A:Cross-references: GB:MS9757; NID:g4897706; PIDN:AAA21271.1; PID:g143391
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Extington, J.; Fabbet, C.; Ferrati, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Toguchi, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.E.; Zumstein, E.; Yoshikawa, H.; Danchin, A. Bacillus subtilis.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A63580; MUID:98044033; PMID:9384377
A:Accession: D69686
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-256 <KUN>
A:Cross-references: GB:Z99112; GB:AL009126; NID:g2633902; PIDN:CAB13427.1; PID:g2633926
A:Experimental source: strain 168
C:Genetics:
A:Gene: pyrDII
C:Superfamily: Pyrococcus furiosus cytochrome-c3 hydrogenase gamma chain

Query Match 7.6%; Score 96.5; DB 2; Length 256;
Best Local Similarity 22.8%; Pred. No. 0.65;
Matches 65; Conservative 32; Mismatches 105; Indels 83; Gaps 14;

QY 1 MKKRVLAICPAALSSQALALVATG---NDTTKEDLVYLNKSEALNSLALIP22PAVGS 57
DB 1 MKKAYLTVCSNQIADRVFQVVLKGELVGQFTTPGQFLHLKVSEAVT---PLLRRLPISIA 58

QY 58 IAFINDQA--NY---EQRLRLNTERGKLAEDANLSSGGVAN-----AFSGAFG 102
DB 59 VNFKEVETIYRVDCGTRLLSKQOGLVDVLGFLNGFPVNEVQPKTALLVGGVG 118

QY 103 SPTEKDPALHKLNTNIEDAGD----LATRSADKHMYRIRPFYFGVSTCNTTQDKL 158
DB 119 -----VPELQELSKLIEKGVNVHVLGFSKND-----VFYEBCRGYGGTYVA 163

QY 159 SKNGSPSGHTSIGWATLV-----VLAENPORONEILKRGYE-----LQSRV 203
DB 164 TADGSY--GET--GVTVDVIRKKLEFDLLSCGTPMLKALKQVAKHKEVLSMERWG 219

QY 204 CGYHWQSDVDAARVGSVAVATHTN-----PAFQQQ 235
DB 220 CG-----IGACFACVCHNESETSVYKVLCDGPVFAQ 252

RESULT 15
D82070
conserved hypothetical protein VC2488 [imported] - Vibrio cholerae (strain N16961 serogr
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Jun-2003
C:Accession: D82070
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
J.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82070
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-178 <HEI>
A:Cross-references: GB:AE004318; GB:AE003852; NID:g9657063; PIDN:AAF95630.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC2488
A:Map position: 1
C:Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain hom

Query Match 7.5%; Score 96; DB 2; Length 178;
Best Local Similarity 31.0%; Pred. No. 0.44;
Matches 27; Conservative 14; Mismatches 42; Indels 4; Gaps 1;

QY 133 KDHYMRIRPFYFGVSTCNTTQDKLSKNGSPSGHTSIGWATLVLAENPORONEILK 192

Db 81 KNSFQRRRPOELSAJATYITPSDRY----SLESGHTAAAFVMAFLIGYIYPHWYAVALC 136

Qy 193 RGYELGQSRVICGYHWCSDVDAARVWG 219

Db 137 WAGLIGLARVLLGVHFLSDVIAGALLG 163

Search completed: June 2, 2004, 10:47:30
Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2004, 10:39:23 ; Search time 18 Seconds
(without alignments)
720.304 Million cell updates/sec

Title: US-09-807-990-2

Perfect score: 1276

Sequence: 1 MKGVV...CPAALFSSQALA.....PAFQQQLQKAKAEPAHQKK 249

Scoring table:

BLOSUM62

Gapop 16.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1014	79.5	249	1	PHOC MORMO
2	1013	79.4	248	1	PHON PROST
3	486	38.1	250	1	PHON SALTY
4	477	37.4	250	1	PHON SALTY
5	339.5	26.6	264	1	PPA ZYMOM
6	96.5	7.6	256	1	PPYK BACSU
7	96	7.5	809	1	HRPB_ECOLI
8	89.5	7.0	1157	1	PEX1_PICPA
9	88	6.9	921	1	NAC2_HUMAN
10	86.5	6.8	390	1	ISDF_BRUSU
11	86	6.7	725	1	RNR_MYCPU
12	86	6.7	1573	1	AROI_SCHPO
13	85.5	6.7	390	1	ISDF_BRUME
14	85	6.7	1603	1	FSC_DROME
15	82.5	6.5	561	1	VGLF_SV41
16	82.5	6.5	898	1	UBPE_DROME
17	82.5	6.5	921	1	NAC2_RAT
18	81.5	6.4	455	1	ODO2_PIG
19	81.5	6.4	2796	1	CSM3_MOUSE
20	81.5	6.4	3670	1	CSM3_HUMAN
21	80.5	6.3	473	1	HN3A_HUMAN
22	80.5	6.3	486	1	YU69_YERPE
23	80.5	6.3	2206	1	POLG_POL3L
24	80	6.3	301	1	MPEV_SYNPF
25	80	6.3	376	1	MURG_RICCN
26	80	6.3	511	1	PUR9_SYNY3
27	80	6.3	953	1	FN33_MOUSE
28	79.5	6.2	232	1	XOHB_ECOLI
29	79.5	6.2	453	1	ODO2_HUMAN
30	79.5	6.2	732	1	POK_DROME
31	79.5	6.2	750	1	YKS7_YEAST
32	79.5	6.2	3746	1	ACVS_PENCH
33	79.5	6.2	3791	1	ACVT_PENCH

ALIGNMENTS

RESULT 1

ID	PHOC MORMO	STANDARD;	PRT;	249 AA.
AC	P28581;			
BT	01-DEC-1992 (Rel. 24, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Major phosphate-irrepressible acid phosphatase precursor (EC 3.1.3.2)			
DE	(HPAP).			
GN	PHOC.			
OS	Morganella morganii (Proteus morganii).			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Morganella.			
OX	NCBI_TaxID=582;			
EN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 21-40.			
RC	STRAIN=RS12;			
EX	MEDLINE=94362901; PubMed=8081499;			
EA	Thaller M.C., Berlutti F., Schippa S., Lombardi G., Rossolini G.M.;			
ET	"Characterization and sequence of Phoc, the principal phosphate-			
RT	irrepressible acid phosphatase of Morganella morganii.";			
RL	Microbiology 140:1341-1350 (1994).			
EN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NCIMB 10466;			
EX	MEDLINE=20336426; PubMed=10877772;			
EA	Mihara Y., Utagawa T., Yamada H., Asano Y.;			
ET	"Phosphorylation of nucleosides by the mutated acid phosphatase from			
RT	Morganella morganii.";			
RL	Appl. Environ. Microbiol. 66:2811-2816 (2000).			
CC	-!- FUNCTION: HAS A PH OPTIMUM AROUND 6.			
CC	-!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an			
CC	alcohol + phosphate.			
CC	-!- SUBUNIT: Homotetramer.			
CC	-!- SUBCELLULAR LOCATION: Periplasmic.			
CC	-!- SIMILARITY: Belongs to the class A bacterial acid phosphatase			
CC	family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X64444; CAA45774.1; -			
DR	EMBL; AB035805; BAA96744.1; -			
DR	PIR; S19187; S19187			
DR	InterPro; IPR008934; ACPase_VanPerase.			
DR	InterPro; IPR001011; Bac_AcPaseA.			
DR	InterPro; IPR000326; PA_PTPase.			
DR	PIfam; PF01569; PAP2; 1.			
DR	PRINTS; PR00483; BACPHPTASE.			
DR	ProDom; PD009838; Bac_AcPaseA; 1.			
DR	SMART; SM00014; acidPpC; 1.			

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DR PROSITE; PS01157; ACID PHOSPH CL A; 1.
KW Hydrolase; Periplasmic; Signal.
FT SIGNAL 1 20
FT CHAIN 21 249 MAJOR PHOSPHATE-IRREPRESSIBLE ACID
SEQUENCE 249 AA; 26998 MW; C43F3698052B6A5C CRC64;
PHOSPHATASE.
Query Match 79.5%; Score 1014; DB 1; Length 249;
Best Local Similarity 77.1%; Pred. No. 7.3e-83;
Matches 192; Conservative 23; Mismatches 34; Indels 0; Gaps 0;
QY 1 MKKRVAVCTAALFSSCALALVATGNDTTTKPDLYLKNSEAINSLALLPPPAVGSIAF 60
DB 1 MKKRVAVCTAALFSSCALALVATGNDTTTKPDLYLKNSEAINSLALLPPPAVGSIAF 60
QY 61 LNDQMYEQGLRNTERRGKLAADANLSSGGVANAFAFGSPITTEKDAPELHKLITNM 120
DB 61 LNDQMYEQGLRNTERRGKLAADANLSSGGVANAFAFGSPITTEKDAPELHKLITNM 120
QY 121 IEDAGDLATRSKADHYMRIRPFYGVSTNTTTEQDKLSXNGSVPSGHTSIGWATALVLA 180
DB 121 IEDAGDLATRSKADHYMRIRPFYGVSTNTTTEQDKLSXNGSVPSGHTSIGWATALVLA 180
QY 181 EIMPQONEILKRGYELGQSRVTCGYHWSQDVDAARVVGSAVATLHTNPAFOOQLOKAK 240
DB 181 EIMPQONEILKRGYELGQSRVTCGYHWSQDVDAARVVGSAVATLHTNPAFOOQLOKAK 240
QY 241 AEFQHQK 249
DB 241 AEFQHQK 249
RESULT 2
PEON PROST
ID PHON PROST STANDARD; PRT; 248 AA.
AC E26975;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nonspecific acid phosphatase precursor (EC 3.1.3.2) (NSAP).
GN PHON.
OS Providencia stuartii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Providencia.
OX NCBI_TaxID=588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PV81;
RA Riccio M.L., Lombardi G., Chiesurin A., Satta G.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate.
CC -|- SUBCELLULAR LOCATION: Periplasmic.
CC -|- SIMILARITY: Belongs to the class A bacterial acid phosphatase
CC family.
-----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.ebi.ac.uk/ebis/sequence/sequence.html
CC or send an email to license@ebi.ac.uk).
-----
CC EXBL; X64820; CAA46032.1; -.
DR EBL; S19888; PAFQCS.
DR InterPro; IPR008934; AcPase VanPerase.
DR InterPro; IPR001011; Bac AcPaseA.
DR InterPro; IPR000326; PAFrase.
DR Pfam; PF01569; PAP2; 1.
DR PRINTS; PR03483; BACPHTASE.
DR ProDom; PD009838; Bac AcPaseA; 1.
DR SMART; SMC0014; acidPPc; 1.
```

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DR PROSITE; PS01157; ACID PHOSPH CL A; 1.
KW Hydrolase; Periplasmic; Signal.
FT SIGNAL 1 20
FT CHAIN 21 248 NONSPECIFIC ACID PHOSPHATASE.
SEQUENCE 248 AA; 27043 MW; 2122A4B95E767CB2 CRC64;
Query Match 79.4%; Score 1013; DB 1; Length 248;
Best Local Similarity 77.4%; Pred. No. 9e-83;
Matches 192; Conservative 26; Mismatches 30; Indels 0; Gaps 0;
QY 1 MKKRVAVCTAALFSSCALALVATGNDTTTKPDLYLKNSEAINSLALLPPPAVGSIAF 60
DB 1 MKKRVAVCTAALFSSCALALVATGNDTTTKPDLYLKNSEAINSLALLPPPAVGSIAF 60
QY 61 LNDQMYEQGLRNTERRGKLAADANLSSGGVANAFAFGSPITTEKDAPELHKLITNM 120
DB 61 LNDQMYEQGLRNTERRGKLAADANLSSGGVANAFAFGSPITTEKDAPELHKLITNM 120
QY 121 IEDAGDLATRSKADHYMRIRPFYGVSTNTTTEQDKLSXNGSVPSGHTSIGWATALVLA 180
DB 121 IEDAGDLATRSKADHYMRIRPFYGVSTNTTTEQDKLSXNGSVPSGHTSIGWATALVLA 180
QY 181 EIMPQONEILKRGYELGQSRVTCGYHWSQDVDAARVVGSAVATLHTNPAFOOQLOKAK 240
DB 181 EIMPQONEILKRGYELGQSRVTCGYHWSQDVDAARVVGSAVATLHTNPAFOOQLOKAK 240
QY 241 AEFQHQK 248
DB 241 AEFQHQK 248
RESULT 3
PHON SALTY
ID PHON SALTY STANDARD; PRT; 250 AA.
AC E26976;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nonspecific acid phosphatase precursor (EC 3.1.3.2) (NSAP).
GN PHON OR STM4319.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14028;
RC MEDLINE=92224869; PubMed=1339343;
RA Groisman E.A., Saier M.H. Jr., Ochman H.;
RT "Horizontal transfer of a phosphatase gene as evidence for mosaic
RT structure of the Salmonella genome."
RL EMBO J. 11:1309-1316(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RC MEDLINE=92041557; PubMed=1938882;
RA Kasahara M., Nakata A., Shinagawa H.;
RT "Molecular analysis of the Salmonella typhimurium phoN gene, which
RT encodes nonspecific acid phosphatase."
RL J. Bacteriol. 173:6760-6765(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RC MEDLINE=21534949; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Dante M., Du F., Hou S., Layman D.,
RA Courtney L., Porwollik S., Ali J., Holmes A., Grewal N., Mulvaney E.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Miller W., Stoneking T., Nhan M.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
CC -|- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
```

```

CC alcohol + phosphate.
CC -!- SUBUNIT: Homodimer (Probable).
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- SIMILARITY: Belongs to the class A bacterial acid phosphatase
CC family.
CC -!- CAUTION: Ref.2 sequence differs from that shown in the C-terminus
CC due to a frameshift.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X63599; CAA45144.1; -.
DR EMBL; X59036; CAA41760.1; ALT_FRAME.
DR EMBL; AE008902; AAL23143.1; -.
DR PIR; S20958; A41330.
DR STYGene; SG10292; phoN.
DR InterPro; IPR008934; AcPase VanPerase.
DR InterPro; IPR001011; Bac AcPaseA.
DR InterPro; IPR000326; PA_FTPase.
DR Pfam; PF01563; PAP2; 1.
DR PRINTS; PR02483; BACPHPTASE.
DR PRODom; PD003838; Bac AcPaseA; 1.
DR SMART; SM00014; acidPPc; 1.
DR PROSITE; PS01157; ACID_PHOSPH_CLA; 1.
KW Hydrolase; Periplasmic; Signal; Complete proteome.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 250 NONSPECIFIC ACID PHOSPHATASE.
SQ SEQUENCE 250 AA; 28382 MW; CFE8DA409D57573 CRC64;
Query Match 38.1%; Score 486; DB 1; Length 250;
Best Local Similarity 43.0%; Pred. No. 5.3e-36;
Matches 104; Conservative 33; Mismatches 99; Indels 10; Gaps 2;
Qy 1 MKKRLVAVCFALFSSQALALVATGNDTTTTKPOLYLLKNSAINSLALLPPPPAVGSIAP 60
Db 1 MRSRYLFFELIVAKYTS-----ETVQP---FHSPESVNSQFVLPFPFGNDPAP 50
Qy 61 LNDQMYEQGLLRNTERGKLAEDANLSSGGVANAFSGAFGSPITEKDAIPALHKLINM 120
Db 51 RYDEAYFKGYAIGKSPRWKQAEADVSVENIARIFSPVVGAKINPKDTPETWMLKNL 110
Qy 121 IEDAGDLATRSADKHMYRIRPFYFGVSTGNTTQDKLSKNGSPSGHTSGMATAVLVA 180
Db 111 LTMGYYATASAKYMYRTFVFNHSTCRPEENTLRKNGSPSGHTAYGTLIALVLS 170
Qy 181 EINPQRNEILKRGYELGQSRVICGYHMQSDVDAARVVGVSAVATLHTNPAFQQLQAK 240
Db 171 EARDPQAELARQWFGQSRVICGALHMQSDVDAAGRYVGVEFARLQTIAPAFQSLAKVR 230
Qy 241 AE 242
Db 231 EE 232
RESULT 4
PHON SALT1
ID PHON_SALT1 STANDARD; PRT; 250 AA.
AC Q934J6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nonspecific acid phosphatase precursor (EC 3.1.3.2) (NSAP).
GN PHON OR STY4519 CR T4225.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OC NCBI_TaxID=601;
RN [1]

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```

RP SEQUENCE FROM N.A.
RA Rao A.S., Mukhopadhyaya R., Mahajan S.K.;
RT "phoN, a gene for acid phosphatase from Salmonella typhi.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wair J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Periplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the class A bacterial acid phosphatase
CC family.
CC -----
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CC -----
DR EMBL; AF366353; AAKS0861.1; -.
DR EMBL; AL627282; CAD09303.1; -.
DR EMBL; AE016848; AAO71687.1; -.
DR InterPro; IPR008934; Bac AcPase VanPerase.
DR InterPro; IPR001011; Bac AcPaseA.
DR InterPro; IPR000326; PA_FTPase.
DR Pfam; PF01569; PAP2; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR PRODom; PD009838; Bac AcPaseA; 1.
DR SMART; SM00014; acidPPc; 1.
DR PROSITE; PS01157; ACID_PHOSPH_CLA; 1.
KW Hydrolase; Periplasmic; Signal; Complete proteome.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 250 NONSPECIFIC ACID PHOSPHATASE.
SQ SEQUENCE 250 AA; 28459 MW; 02B92D2035F4FE82 CRC64;
Query Match 37.4%; Score 477; DB 1; Length 250;
Best Local Similarity 47.0%; Pred. No. 4e-35;
Matches 95; Conservative 31; Mismatches 76; Indels 0; Gaps 0;
Qy 41 BAINSLALLPPPPAVGSTAFNLNDQMYEQGLLRNTERGKLAEDANLSSGGVANAFSGA 100
Db 31 BSVNSQFVLPFPFGNDPAPFYDKAEYFKGYAIGKSPRWKQAEADVSVENIARIFSPV 90
Qy 101 FGSPIEKDAPALHKLINMIEDAGDLATRSADKHMYRIRPFYFGVSTCNTEDQKLSK 160
Db 91 VGAKINPKDTPETWMLQNLKMGYYATASAKYMYRTFVFNHSTCRPEENTLRK 150
Qy 161 NGSYBSGHTSGMATAVLVAINPQRNEILKRGYELGQSRVICGYHMQSDVDAARVVGS 220
RN [1]

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KAHLER A.E., Nielsen F.S., Switzer R.L.;
"Biochemical characterization of the heteromeric Bacillus subtilis
dihydroxycarboxylate dehydrogenase and its isolated subunits";
Arch. Biochem. Biophys. 371:191-201(1999).
CC -!- FUNCTION: Is responsible for channeling the electrons from the
oxidation of dihydroxycarboxylate from the FMN redox center in the pyrid
subunit to the ultimate electron acceptor NAD(+).
CC -!- COFACTOR: Binds 1 2Fe-2S cluster and 1 FAD per subunit.
CC -!- PATHWAY: Pyrimidine biosynthesis; fourth step.
CC -!- SUBUNIT: Heterotetramer of 2 pyrK and 2 pyrd subunits.
CC -!- SIMILARITY: Belongs to the pyrK family.
CC
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CC
EMBL; M59757; AAA21271.1; --
DR EMBL; Z99112; CAB13427.1; --
DR PIR; G39845; G39845.
DR Subtilist; BG10717; pyrK.
DR HAMAP; MF 01211; -- 1.
DR InterPro; IPR006058; 2Fe2S fd BS.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00175; NAD binding_1; 1.
DR PROSITE; PS0197; 2FE2S_FERREDOXIN; FALSE NEG.
KW Pyrimidine biosynthesis; transport; Electron transport; Metal-binding;
KW Iron; iron-sulfur; 2Fe-2S; Flavoprotein; FAD; Complete proteome.
FT METAL 220 220 IRON-SULFUR 1 (2FE-2S) (PROBABLE).
FT METAL 225 225 IRON-SULFUR 1 (2FE-2S) (PROBABLE).
FT METAL 228 228 IRON-SULFUR 2 (2FE-2S) (PROBABLE).
FT METAL 243 243 IRON-SULFUR 2 (2FE-2S) (PROBABLE).
SQ SEQUENCE 256 AA; 28099 MW; DCTB7605E39C2E15 CRC64;
Query Match 7.6%; Score 96.5; DB 1; Length 256;
Best Local Similarity 22.8%; Pred. No. 0.27;
Matches 65; Conservative 32; Mismatches 105; Indels 83; Gaps 14;
QY 1 MKKRVLAFCFAALFSSQALVALVATG---NDTTFEDLYLKNSEAINSLALLPPPPAVGS 57
DB 1 MKKAYLATVCSNQIADRFVFMVKGELVQGTTPGQFLHLKVSEAVT--PLLRREPISTAD 58
58 IAFLENDQA--WY-----EQGLLRNTERCKLAEDANLSSGGVAN-----AFSGAFG 102
59 VNFKEVETIYRVDGEGTRLSLKQGLVWV-LGPLNGFPVNEVQPKTALLVGGVG 118
103 SPITEKDAPALHKLITNMIEDAGD---LATASAKDHYMRIRPFYGVSTNTTEQDKL 158
119 -----VPPQLQELSKRLIEKGVNVIHVLGFQSAKD-----VFYECKRQYGDITYVA 163
159 SSKGYSYSGHTSIGWATL-----VLAENPQRONEILKRCYE-----LQQRVVI 203
164 TADGSGY--GET--GEFTDVIKRLKLEFDILLSGCGPTMLKALKQBYAHKVVYLSMEERMG 219
204 CGYHWQSDVDAARVVGSAVAVATLNTN-----PAFQQQ 235
220 CG-----IGACFACVCHTNESETSYVKVCLDGPVFKAQ 252
RESULT 7
ID HRPB_ECOLI STANDARD; PRT; 809 AA.
AC P37024; P75663;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE ATP-dependent helicase hrpB.
GN HRPB OR B0148.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
[1] SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / W3110;
RX MEDLINE=94261430; PubMed=8202364;
RA Fujita N., Mori H., Yura T., Ishihama A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of
the 2.4-4.1 min (110,917-193,643 bp) region.";
RL Nucleic Acids Res. 22:1637-1639(1994).
[2] SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Valdes J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
[3] SEQUENCE OF 61-156 FROM N.A.
RP STRAIN=K12 / W3110;
RX MEDLINE=95206938; PubMed=7899078;
RA Moriya H., Kasai H., Isono K.;
RT "Cloning and characterization of the hrpA gene in the terC region of
Escherichia coli that is highly similar to the DEAH family RNA
helicase genes of Saccharomyces cerevisiae.";
RL Nucleic Acids Res. 23:595-598(1995).
CC -!- SIMILARITY: TO EUKARYOTIC RNA HELICASES; STRONGEST SIMILARITY
TO YEAST DHR.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to
frameshifts.
CC
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or send an email to license@isb-sib.ch).
CC
EMBL; D26562; --; NOT ANNOTATED CDS.
DR EMBL; AE000124; AAC73259.1; ALT_INIT.
DR EMBL; D42122; BAA21040.1; --
DR EcoGene; EG12329; hrpB.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF04408; HA2; 1.
DR Pfam; PF00271; helicase_C; 1.
DR SMART; SM03487; DEXDC; 1.
DR SMART; SM03490; HELICC; 1.
KW Helicase; ATP-binding; Complete proteome.
FT NP_BIND 27 34 ATP (POTENTIAL).
FT SITE 123 126 DEFB BOX.
SQ SEQUENCE 809 AA; 89147 MW; 413605E1D2D90715 CRC64;
Query Match 7.5%; Score 96; DB 1; Length 809;
Best Local Similarity 23.2%; Pred. No. 1.3;
Matches 66; Conservative 33; Mismatches 116; Indels 70; Gaps 13;
QY 3 KRVLAFCFA---ALFSSQALVALVATGNDT--TKPDLYLKNSE-----AINSLALLPPPPAV 55
DB 390 KRLQMLGALGERLSAQCKQMAALGNDPRLAAMLVSAKNDDEAATAKIALLEPEPM 449
QY 56 GS-----IAPLNDQAMYEQ--GRLLNTERGKLAEDANLSSGGVANAFSGAFGSPITEKD 109
DB 450 GNSDVGAVFSPNPAWQQRKSQLLK-----RLNVRGSGEADSLIAPLLAGAFADRIARRR 504
QY 110 APALHKLITN-----MIEDAGDLATRSKADHYMRIRPFYGV----- 146

```
Db 505 GQGRYQLAKEMGAMLDANDALSR-----HEWLIAPLLQLQGSAPDARILALALVLDIVELV 560
Qy 147 -----VSTGNTTQODKLSKNGSVPS-GHTSIGATLV--LA-----EINPQONELIX 192
Db 561 QRCFOLVQSDTVZWD--DAQGLKAWRLQIGQLTKVQPLAKPSDELEHQMGLNGIRD 618
Qy 193 RGY-----ELGQSRVIGYHQSDVDARVVGSAVATLHT 228
Db 619 KGLSVLNTWTAEEQLRLRLCAKWLPEYDWPFAVDDESLLAALET 663

RESULT 8
PEX1_PICPA
ID PEX1_PICPA STANDARD; PRT; 1157 AA.
AC P46463;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Peroxisome biosynthesis protein PAS1 (Peroxin-1).
GN PEX1 OR PAS1.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=21-1;
RX MEDLINE=95050987; PubMed=7962088;
RA Heyman J.A., Monosov E., Subramani S.;
RT "Role of the PAS1 gene of Pichia pastoris in peroxisome biogenesis.";
RL J. Cell Biochem. 127:1259-1273(1994).
CC -1- FUNCTION: Involved in peroxisome biosynthesis. May play a direct
or indirect role in delivering membrane material to developing
peroxisomes. It may also be involved in intracellular membrane
movement.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the AAA ATPase family.

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EMBL: Z36987; CA885450.1; -.
DR PIR; A55152; A55152.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_Centr.
DR InterPro; IPR003960; AAA_sub.
DR Pfam; PF00004; AAA; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00674; AAA; 1.
KW Peroxisome; ATP-binding; Repeat.
FT NP_BIND 523 530 ATP (POTENTIAL).
FT NP_BIND 940 947 ATP (POTENTIAL).
SQ SEQUENCE 1157 AA; 126984 MW; B26F46F5FA92DA3C CRC64;

Query Match 7.0%; Score 89.5; DB 1; Length 1157;
Best Local Similarity 21.2%; Pred. No. 5.1; Indels 79; Gaps 12;
Matches 55; Conservative 40; Mismatches 86;

Qy 25 GNDTTTQPD-----LYLKNSEAINSLALPPPPAVGSIATFLNDQAMYEQGRLL----- 72
Db 909 GHDSGTGTVDRVWQMLQMDAGELDGVYVL---AATSRLDLSALLRPRGLDKSVIC 964
Qy 73 -----LRNTERGKLAEDANILSS-GGVANAFSGAPGSPITEKQAPAL----- 113
Db 965 DMPEDFDRELDILQSVTRNMYVSKSVNLSSVAGSGSGFSGA-----DLQALAYNAYLK 1016
Qy 114 --HKILF--KNIEDAGLPLATSAKDHYRIRPFAYGVSTCTWTTEQDKLSKNGSVPSGHT 169
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Db 1017 AVHEKLLTKDESMAMAGEKDND--DKRMVSCFQFSG-----NTEKKS----- 1057
Qy 170 SIGWATALVLAERINPQRQNEILKRGYELGQSRVIGYHQSDVDARVVGSAVATLHTN 229
Db 1058 -----LIELKPSDRATVVKLEHLYQGN---GNHAGET-KSKLATTANSVIITS 1104
Qy 230 PAFQOQLQXKAKAEFAHQKK 249
Db 1105 KDFEDSLSETKQSIQSEKR 1124

RESULT 9
NAC2_HUMAN
ID NAC2_HUMAN STANDARD; PRT; 921 AA.
AC Q9UPR5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sodium/calcium exchanger 2 precursor (Na(+)/Ca(2+)-exchange protein
2).
GN SLC8A2 OR NCX2 OR KIAA1087.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99397452; PubMed=10470851;
RA Kituno R., Nagase T., Ishikawa K.-I., Hirose M., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIV.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
RL DNA Res. 6:197-205(1999).
CC -1- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
coupling. Ca(2+) is extruded from the cell during relaxation so as
to prevent overloading of intracellular stores (By similarity).
CC -1- ENZYME REGULATION: By ATP (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

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EMBL: AB029010; BA83039.1; ALT_INIT.
DR GenBank; HGNC; 11069; SLC8A2.
DR MIM; 601901; -.
DR InterPro; IPR003644; Calx_beta.
DR InterPro; IPR004836; Na_Ca_Ex.
DR InterPro; IPR004837; NaCa_Extrem.
DR Pfam; PF03160; Calx-beta; 2.
DR Pfam; PF01699; Na_Ca_Ex; 2.
DR PRINTS; PR01259; NACAEXCHNGR.
DR SMART; SM00237; Calx_beta; 2.
DR TIGRFAms; TIGR00845; caca; 1.
KW Transport; Antiport; Calcium transport; Sodium transport;
Transmembrane; Glycoprotein; Phosphorylation; Signal;
KW Calmodulin-binding; Repeat.
FT SIGNAL 1 20
FT CHAIN 21 921
FT DOMAIN 21 68 SODIUM/CALCIUM EXCHANGER 2.
FT TRANSMEM 69 90 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 91 130 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 131 152 POTENTIAL.
FT TRANSMEM 153 164 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 165 185 POTENTIAL.
FT TRANSMEM 186 196 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 197 219 POTENTIAL.
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QY 245 QHOKK 249
DB 306 EHAOK 310

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RESULT 11
ID_RNR_MYCPU STANDARD; PRT; 725 AA.
AC Q98QLO;
DE 28-FEB-2003 (Rel. 41, Created)
DE 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease R (EC 3.1.-.-) (RNase R) (VacB protein homolog).
GN RNR OR VACB OR MYPU 35:0.
CS Mycoplasma pulmonis.
CC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
CX NCBI_TaxID=2107;
RN SEQUENCE FROM N.A.
RP STRAIN=UAB CTIP;
RC MEDLINE=21267165; PubMed=11353084;
RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA Blanchard A.;
RT "The complete genome sequence of the murine respiratory pathogen
RT Mycoplasma pulmonis."
RL Nucleic Acids Res. 29:2145-2153(2001).
CC -1- FUNCTION: 3'-5' exoribonuclease that participates in an essential
CC cell function. Acts nonspecifically on poly(A), poly(U) and
CC ribosomal RNAs (By similarity).
CC -1- SIMILARITY: Belongs to the ribonuclease II (RNB) family.
CC -1- SIMILARITY: Contains 1 SI motif domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AL445564; CAC13524.1; -.
CC PIR: G90555; G90555.
CC DR Mypulist; MYPU 3510; -.
CC DR InterPro; IPR004476; 3 prime RNase.
CC DR InterPro; IPR008994; Nucleic acid OB.
CC DR InterPro; IPR001900; Ribonuclease_II.
CC DR InterPro; IPR003029; SI.
CC DR Pfam; PF00773; RNB; 1.
CC DR Pfam; PF00575; SI; 1.
CC DR SMART; SM00316; SI; 2.
CC DR TIGRFAMs; TIGR00358; 3 prime RNase; 1.
CC DR PROSITE; PS01175; RIBONUCLEASE_II; 1.
CC DR PROSITE; PS0126; SI; 1.
CC DR Hydrolase; Exonuclease; Nuclease; RNA-binding; Complete proteome.
FT DOMAIN 611 689 SI MOTIF.
SQ SEQUENCE 725 AA; 83720 MW; FF734E9E7D27A5CD CRC64;

Query Match 6.7%; Score 86; DB 1; Length 725;
Best Local Similarity 24.0%; Pred. No. 9;
Matches 35; Conservative 22; Mismatches 55; Indels 24; Gaps 4;

QY 14 FSSQALVAVAGNDTTTKPOLYLNKSEAINSLA-----LPPFAVGSIAFLN 62
DB 434 FVNRANAVAKNNKLLPSIYRVHDPSTESLFLFKTLTLGIDFTPKITSPKAFSD 493
QY 63 DQMYEFG-----RLRNTREKGLADEANILSSGVANAFSGAFGSPITEKDALP 113
DB 494 SFEEKIKQYQIDNFVKLVLTMTB--KAIVSDKNIGHFGLASSYSHFTSIRYPLQL 551
QY 114 HKLLTNMIEDAGDLATRSADKHVMRI 139
DB 552 HRLIKQWFEKSNL--KEKNHFSLI 575
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RESULT 12
ID_ARO1_SCHPO STANDARD; PRT; 1573 AA.
AC Q9PFR0;
DE 16-OCT-2001 (Rel. 40, Created)
DE 16-OCT-2001 (Rel. 40, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pentafunctional AROM polypeptide [Includes: 3-dehydroquinase synthase
DE (EC 4.2.3.4); 3-dehydroquinase dehydratase (EC 4.2.1.10) (3-
DE dehydroquinase); Shikimate 5-dehydroquinase (EC 1.1.1.25); Shikimate
DE kinase (EC 2.7.1.71); 3-phosphoshikimate 1-carboxyvinyltransferase
DE (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP
DE synthase) (EPSPS)].
GN ARO1 OR SPAC1834.02.
CS Schizosaccharomyces pombe (Fission yeast).
CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
CC Schizosaccharomycetales; Schizosaccharomycetaceae;
CC Schizosaccharomycetes.
CX NCBI_TaxID=4896;
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RC MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris P., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett E., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymoprez B.,
RA Weidjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann M., Medler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCorbie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -1- FUNCTION: The AROM polypeptide catalyzes 5 consecutive enzymatic
CC reactions in prechorismate polyaromatic amino acid biosynthesis
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: 3-deoxy-arabino-heptulosonate 7-phosphate = 3-
CC dehydroquinase + phosphate.
CC -1- CATALYTIC ACTIVITY: 3-dehydroquinase = 3-dehydroshikimate + H(2)O.
CC -1- CATALYTIC ACTIVITY: Shikimate + NADP(+) = 5-dehydroshikimate +
CC NADPH.
CC -1- CATALYTIC ACTIVITY: ATP + shikimate = ADP + shikimate 3-phosphate.
CC -1- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC second step.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC third step.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC fourth step.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC fifth step.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC sixth step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 10:38:48 ; Search time 61 Seconds
(without alignments)
1153.350 Million cell updates/sec

Title: US-09-807-990-2

Perfect score: 1276

Sequence: 1 MKREVLAVCAALFSSQALA.....PAFQQQLQKAKAEFAQHKK 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1276	100.0	249	2 AAW06463	Escherich
2	1276	100.0	249	2 AAW71029	Acid phos
3	1276	100.0	249	4 AAB75064	Escherich
4	1183	92.7	231	2 AAW71034	Mutant ac
5	1178	92.3	231	2 AAW71035	Mutant ac
6	1161	91.0	231	2 AAW71036	Mutant ac
7	1158	90.8	248	2 AAW06458	Enterobac
8	1158	90.8	248	2 AAW71031	Acid phos
9	1152	90.3	231	2 AAW71037	Mutant ac
10	1152	90.3	231	2 AAW71038	Mutant ac
11	1143	89.6	248	2 AAW06459	Klebeieil
12	1143	89.6	248	2 AAW71032	Acid phos
13	1141	89.4	231	2 AAW71039	Mutant ac
14	1137	89.1	231	2 AAW71040	Mutant ac
15	1133	88.8	231	2 AAW71041	Mutant ac
16	1129	88.5	231	2 AAW71042	Mutant ac
17	1112	87.1	248	4 AAB75068	Enterobac
18	1014	79.5	249	2 AAW06462	Morganell
19	1014	79.5	249	2 AAW71028	Acid phos
20	1014	79.5	249	4 AAB75065	Morganell
21	1013	79.4	248	2 AAW06457	Providenc
22	1013	79.4	248	2 AAW71030	Acid phos
23	973	76.3	249	4 AAU27583	Fusion pr
24	780	61.1	244	2 AAW06460	Serratia
25	780	61.1	244	2 AAW71033	Acid phos

26	591	46.3	246	2 AAR54082	Virulence
27	586	45.9	246	2 AAR35759	Apvriase
28	481	37.7	232	4 AAB75066	Salmonell
29	339.5	26.6	264	4 AAB75067	Zymomonas
30	314.5	24.6	252	2 AAR20014	Ascorbic
31	149.5	11.7	508	4 AAU56365	Propionib
32	149.5	11.7	508	6 AAB52884	Propionib
33	143	11.2	622	4 AAG91063	C glutami
34	130.5	10.2	513	5 ABP65275	Bifidobac
35	105	8.2	58	5 ABP08795	Human ORF
36	96	7.5	178	6 ABU49566	Protein e
37	96	7.5	824	4 AAG98907	E. coli g
38	96	7.5	824	6 ABU14676	Protein e
39	95	7.4	855	4 ABB29301	Novel hum
40	93.5	7.3	704	6 ABB80170	A. fumiga
41	92.5	7.2	159	4 AAB76560	Corynebac
42	92.5	7.2	159	4 AAG92925	C glutami
43	92	7.2	398	6 ABB70672	Phototrab
44	90.5	7.1	437	6 ABU38661	Protein e
45	90.5	7.1	578	4 ABB71754	Drosophil

ALIGNMENTS

RESULT 1
AAW06463
ID AAW06463 standard; protein; 249 AA.
AC AAW06463;
XX
XX 13-AUG-1997 (first entry)
XX
DE Escherichia blattae JCM 1650 acid phosphatase.
XX
XX JCM 1650; acid phosphatase; production; nucleoside; 5'-phosphate; ester;
KW condiment; pharmaceutical; intermediate.
XX
OS Escherichia blattae.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..18
FT Peptide /label= sig_peptide
FT Peptide 19..249
FT Misc-difference 92 /label= mat_peptide
FT Misc-difference 171 /note= "optionally replaced by another amino acid"
FT Misc-difference 171 /note= "optionally replaced by another amino acid"

WO9637603-A1.

28-NOV-1996.

24-MAY-1996; 96WO-JP001402.

25-MAY-1995; 95JP-00149781.

26-MAY-1996; 96JP-00094680.

(AJIN) AJINOMOTO CO INC.

Mihara Y, Utagawa T, Yamada H, Asano Y;

WPI; 1997-021215/02.

N-PSDB; AAT45011.

Efficient production of nucleoside 5'-phosphate - by reaction of a nucleoside with a phosphoric acid donor in the presence of an acid phosphatase.

Claim 3; Page 56-58; 95pp; Japanese.

The present sequence is the Escherichia blattae JCM 1650 acid phosphatase

CC (AP), which can be used to produce a nucleoside 5'-phosphate ester from
 CC the corresponding nucleoside when a phosphate donor, e.g. poly-, phenyl-
 CC or carbamyl-phosphoric acid, is reacted in its presence at pH 3.0 to 5.5.
 CC The PA can be used for the economic and efficient production of
 CC nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals and
 CC intermediates for pharmaceuticals
 XX Sequence 249 AA;

Query Match 100.0%; Score 1276; DB 2; Length 249;
 Best Local Similarity 100.0%; Pred. No. 1.3e-128;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKRVLAFCFAALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSI AF 60
 DB 1 MKKRVLAFCFAALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSI AF 60
 QY 61 LNPQAMYEQGRLLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDPALHKLITNM 120
 DB 61 LNPQAMYEQGRLLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDPALHKLITNM 120
 QY 121 IEDAGDLATRSKADHYRIIRPFAYGYSTCNTTTEQDKLSKNGSYPSGHTSIGWATALVLA 180
 DB 121 IEDAGDLATRSKADHYRIIRPFAYGYSTCNTTTEQDKLSKNGSYPSGHTSIGWATALVLA 180
 QY 181 EINPQRONEILKRGYELGQSRVIGYHWSQSDVDARVVGSAVATLTNPAFQOQLOKAK 240
 DB 181 EINPQRONEILKRGYELGQSRVIGYHWSQSDVDARVVGSAVATLTNPAFQOQLOKAK 240
 QY 241 AEPAQHOKK 249
 DB 241 AEPAQHOKK 249

RESULT 2

AAW71029
 ID AAW71029 standard; protein; 249 AA.
 AC AAW71029;
 XX
 XX 21-OCT-1998 (first entry)
 XX
 DE Acid phosphatase enzyme amino acid sequence.
 XX
 KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 KW intermediate.
 XX
 OS Escherichia blattae.

Key Location/Qualifiers
 FE Peptide 1..18
 FT /note= "signal peptide"
 FT P:Protein 19..249
 FT /note= "mature protein; Claim 6"

XX EP857788-A2.
 XX
 XX 12-AUG-1998.
 XX
 XX 20-NOV-1997; 97EP-00309165.
 XX
 XX 21-NOV-1996; 96JP-00321103.
 XX 18-JUN-1997; 97JP-00161674.
 XX
 PA (AJIN) AJINOMOTO CO INC.

XX Mihara Y, Utagawa T, Yamada H, Asano Y;
 XX WP-; 1998-416010/36.
 XX N-PSDB; AAV43046.

PT Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 PT with phosphate donor in presence of acid phosphatase - used as seasonings

or pharmaceutical intermediates.

XX Example 12; Page 35-36; 83pp; English.

CC The present sequence represents an acid phosphatase enzyme. The
 CC specification describes a method for the preparation of nucleoside 5'-
 CC phosphate esters. The method comprises reacting a nucleoside with a
 CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
 CC has been altered to increase its affinity for the nucleoside and/or to
 CC increase its thermal stability, or in the presence of a microorganism
 CC that has been transformed with recombinant DNA containing a gene coding
 CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
 CC seasonings or pharmaceuticals or as intermediates for them

XX Sequence 249 AA;

Query Match 100.0%; Score 1276; DB 2; Length 249;
 Best Local Similarity 100.0%; Pred. No. 1.3e-128;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKKRVLAFCFAALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSI AF 60
 DB 1 MKKRVLAFCFAALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSI AF 60
 QY 61 LNPQAMYEQGRLLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDPALHKLITNM 120
 DB 61 LNPQAMYEQGRLLNTERGKLAEDANLSSGGVANAFSGAFSPITEKDPALHKLITNM 120
 QY 121 IEDAGDLATRSKADHYRIIRPFAYGYSTCNTTTEQDKLSKNGSYPSGHTSIGWATALVLA 180
 DB 121 IEDAGDLATRSKADHYRIIRPFAYGYSTCNTTTEQDKLSKNGSYPSGHTSIGWATALVLA 180
 QY 181 EINPQRONEILKRGYELGQSRVIGYHWSQSDVDARVVGSAVATLTNPAFQOQLOKAK 240
 DB 181 EINPQRONEILKRGYELGQSRVIGYHWSQSDVDARVVGSAVATLTNPAFQOQLOKAK 240
 QY 241 AEPAQHOKK 249
 DB 241 AEPAQHOKK 249

RESULT 3

AAW75064
 ID AAW75064 standard; protein; 249 AA.

AC AAW75064;

XX 23-JUL-2001 (first entry)

XX Escherichia blattae nucleotide-5'-phosphate producing enzyme protein.

XX Variant nucleoside-5'-phosphate producing enzyme; mutagenesis;
 KW transphosphorylation; phosphatase; protein co-ordinate data;
 KW X-ray structural analysis; three-dimensional structure.

XX Escherichia blattae.

XX WC200118184-A1.

XX 15-MAR-2001.

XX 01-SEP-2000; 2000WO-JP005973.

XX 03-SEP-1999; 99JP-00249545.

XX (AJIN) AJINOMOTO CO INC.

XX Istikawa K, Suzuki E, Gondoh K, Shimba N, Mihara Y, Kawasaki H;
 PI Kurahashi O, Kouda T, Shimaoka M, Kozutsumi R, Asano Y;

XX WPI; 2001-380914/40.

XX N-PSDB; AAW19701.

PT Variant enzyme having elevated nucleoside 5'-prime phosphate producing
 PT activity and having a specific three-dimensional structure for production
 of nucleotides as pharmaceutical intermediates.

XX Disclosure; Page 157; 150pp; Japanese.

XX The present invention describes a variant nucleoside-5'-phosphate
 CC producing enzyme which is a modification of a transphosphorylase or
 CC phosphatase which contains a lysine, two arginine and two histidine
 CC residues and in which the C-alpha distances between these residues are
 CC enclosing a space which permits the binding of a nucleoside with these
 CC residues. Also described are: (1) a gene encoding the variant enzyme; (2)
 CC expression vectors containing the DNA; (3) host cells transformed by the
 CC vectors; (4) preparation of the variant enzyme by culture of the
 CC transformants; (5) crystals of the enzyme and of a complex of the enzyme
 CC with molybdenic acid; and (6) selection of inhibitors of acid phosphatase
 CC or transphosphorylase using the structural coordinates derived from the
 CC enzyme. The variant enzymes with increased efficiency for production of
 CC nucleoside 5'-phosphates can be used as pharmaceutical intermediates.
 CC AAB19701 to AAB19785 and AAB75064 to AAB75101 represent sequences used in
 CC the exemplification of the present invention

XX Sequence 249 AA;

Query Match 100.0%; Score 1276; DB 4; Length 249;
 Best Local Similarity 100.0%; Pred. No. 1.3e-128;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKRVLAFCFAALFSSQALALVATGNTTTKPDLYLKNSEAINSLALLPPPAVGSIAF 60
 DB 1 MKKRVLAFCFAALFSSQALALVATGNTTTKPDLYLKNSEAINSLALLPPPAVGSIAF 60
 QY 61 LNDQAMYEQGRLLNTERGKLAEDANLSSGVANAFSGAFSPITEKDAPALHKLNTNM 120
 DB 61 LNDQAMYEQGRLLNTERGKLAEDANLSSGVANAFSGAFSPITEKDAPALHKLNTNM 120
 QY 121 IEDAGDLATRSADKHVMRIRPFYFVSTONTTQDKLSKNGSYPSGHTSIGWATALVLA 180
 DB 121 IEDAGDLATRSADKHVMRIRPFYFVSTONTTQDKLSKNGSYPSGHTSIGWATALVLA 180
 QY 181 EINFQONEILKRGYELGOSRVICGYHWQSDVDAARVWGSVAVATLTHTNPAFOOQLOKAK 240
 DB 181 EINFQONEILKRGYELGOSRVICGYHWQSDVDAARVWGSVAVATLTHTNPAFOOQLOKAK 240
 QY 241 AEFAQHOKK 249
 DB 241 AEFAQHOKK 249

RESULT 4

AAW71034
 ID AAW71034 standard; protein; 231 AA.

AC AAW71034;

XX 21-OCT-1998 (first entry)

DE Mutant acid phosphatase enzyme of Escherichia blattae.

XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 KW mutant; intermediate.

XX Synthetic.

OS Escherichia blattae.

XX Key Location/Qualifiers

PH Misc-difference 74

FT /label= G74D

DN EP857788-A2.

XX 12-AUG-1998.

PD

XX

PF 20-NOV-1997; 97EP-00309365.

XX 21-NOV-1996; 96JP-00311103.

PR 18-JUN-1997; 97JP-00161674.

XX (AJIN) AJINOMOTO CO INC.

PI Mihara Y, Utagawa T, Yamada H, Asano Y;

XX WPI; 1998-416010/36.

DR Preparation of nucleoside 5'-phosphates comprises reacting nucleoside

XX with phosphate donor in presence of acid phosphatase - used as seasonings

PT or pharmaceutical intermediates.

XX Example 19; Page; 83pp; English.

XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were

CC created using the mature protein of AAW71029. The specification describes

CC a method for the preparation of nucleoside 5'-phosphate esters. The

CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-

CC 5.5 in the presence of an acid phosphatase that has been altered to

CC increase its affinity for the nucleoside and/or to increase its thermal

CC stability, or in the presence of a microorganism that has been

CC transformed with recombinant DNA containing a gene coding for such an

CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or

CC pharmaceuticals or as intermediates for them. note: this sequence does

CC not appear in the specification; it was created using information

CC provided

XX Sequence 231 AA;

QY Query Match 92.7%; Score 1183; DB 2; Length 231;

DB Best Local Similarity 99.6%; Pred. No. 1.3e-118;

Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 LALVATGNDTTKPDLYLKNSEAINSLALLPPPAVGSIAFINDQAMYEQGRLLNTER 78

DB 1 LALVATGNDTTKPDLYLKNSEAINSLALLPPPAVGSIAFINDQAMYEQGRLLNTER 60

QY 79 GKLAEDANLSSGVANAFSGAFSPITEKDAPALHKLNTNMIEDAGDLATRSADKHVMR 138

DB 61 GKLAEDANLSSGVANAFSGAFSPITEKDAPALHKLNTNMIEDAGDLATRSADKHVMR 120

QY 139 IRPFYFVSTONTTQDKLSKNGSYPSGHTSIGWATALVLAIEINPQONEILKRGYELG 198

DB 121 IRPFYFVSTONTTQDKLSKNGSYPSGHTSIGWATALVLAIEINPQONEILKRGYELG 180

QY 199 QSRVICGYHWQSDVDAARVWGSVAVATLTHTNPAFOOQLOKAKAEFAQHOKK 249

DB 181 QSRVICGYHWQSDVDAARVWGSVAVATLTHTNPAFOOQLOKAKAEFAQHOKK 231

RESULT 5

AAW71035

ID AAW71035 standard; protein; 231 AA.

XX AAW71035;

XX 21-OCT-1998 (first entry)

DE Mutant acid phosphatase enzyme of Escherichia blattae.

XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;

KW mutant; intermediate.

XX Synthetic.

OS Escherichia blattae.

XX Key Location/Qualifiers

PH Misc-difference 74

FT /label= G74D

FT Misc-difference 153

FT XX
PN XX
XX EP857788-A2. /label= I153T
XX
PD XX
XX 12-AUG-1998.
XX
PF XX
XX 20-NOV-1997; 97EP-00309365.
XX
PR XX
XX 21-NOV-1996; 96JP-00311103.
PR XX
XX 18-JUN-1997; 97JP-00161674.
XX
XX (AJIN) AJINOMOTO CO INC.
XX
XX Mihara Y, Utagawa T, Yamada H, Asano Y;
XX WPI; 1998-416010/36.
XX
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT with phosphate donor in presence of acid phosphatase - used as seasonings
PT or pharmaceutical intermediates.
XX
PS Example 13; Page; 83pp; English.
XX
XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
CC created using the mature protein of AAW71029. The specification describes
CC a method for the preparation of nucleoside 5'-phosphate esters. The
CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
CC 5.5 in the presence of an acid phosphatase that has been altered to
CC increase its affinity for the nucleoside and/or to increase its thermal
CC stability, or in the presence of a microorganism that has been
CC transformed with recombinant DNA containing a gene coding for such an
CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
CC pharmaceuticals or as intermediates for them. note: this sequence does
CC not appear in the specification; it was created using information
CC provided
XX
XX Sequence 231 AA;
SQ
Query Match 92.3%; Score 1178; DB 2; Length 231;
Best Local Similarity 99.1%; Pred. No. 4.4e-118;
Matches 229; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 19 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAPFLNDQAMYEQGLLRNTER 78
Db 1 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAPFLNDQAMYEQGLLRNTER 60
QY 79 GKLAEDANLSSGGVANAFSGAFSPITEKDAPALHKLITNMIEDAGDLATRSKDHVYR 138
Db 61 GKLAEDANLSSGGVANAFSGAFSPITEKDAPALHKLITNMIEDAGDLATRSKDHVYR 120
QY 139 IRPFAFGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPNQONELKRGYELG 198
Db 121 IRPFAFGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPNQONELKRGYELG 180
QY 199 QSRVICGYHWQSDVDAARVGSVAVVATLHTNPAFCQQLOKAKAEFAQHKK 249
Db 181 QSRVICGYHWQSDVDAARVGSVAVVATLHTNPAFCQQLOKAKAEFAQHKK 231
RESULT 6
AAW71036
ID AAW71036 standard; protein; 231 AA.
XX
AC AAW71036;
XX
DT 21-OCT-1998 (first entry)
XX
DE Mutant acid phosphatase enzyme of Escherichia blattae.
XX
KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
KW mutant; intermediate.
XX
OS Synthetic.

OS Escherichia blattae.
XX
FH Key Location/Qualifiers
FT Misc-difference 63 /label= L63Q
FT Misc-difference 65 /label= A65Q
FT Misc-difference 66 /label= E66A
FT Misc-difference 74 /label= G74D
FT Misc-difference 153 /label= I153T
FT
XX EP857788-A2.
XX
XX 12-AUG-1998.
XX
XX 20-NOV-1997; 97EP-00309365.
XX
XX 21-NOV-1996; 96JP-00311103.
PR
XX 18-JUN-1997; 97JP-00161674.
XX
XX (AJIN) AJINOMOTO CO INC.
XX
XX Mihara Y, Utagawa T, Yamada H, Asano Y;
XX WPI; 1998-416010/36.
XX
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT with phosphate donor in presence of acid phosphatase - used as seasonings
PT or pharmaceutical intermediates.
XX
XX Example 13; Page; 83pp; English.
XX
XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
CC created using the mature protein of AAW71029. The specification describes
CC a method for the preparation of nucleoside 5'-phosphate esters. The
CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
CC 5.5 in the presence of an acid phosphatase that has been altered to
CC increase its affinity for the nucleoside and/or to increase its thermal
CC stability, or in the presence of a microorganism that has been
CC transformed with recombinant DNA containing a gene coding for such an
CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
CC pharmaceuticals or as intermediates for them. note: this sequence does
CC not appear in the specification; it was created using information
CC provided
XX
XX Sequence 231 AA;
SQ
Query Match 91.0%; Score 1161; DB 2; Length 231;
Best Local Similarity 97.8%; Pred. No. 3e-116;
Matches 226; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 19 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAPFLNDQAMYEQGLLRNTER 78
Db 1 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAPFLNDQAMYEQGLLRNTER 60
QY 79 GKLAEDANLSSGGVANAFSGAFSPITEKDAPALHKLITNMIEDAGDLATRSKDHVYR 138
Db 61 GKLAEDANLSSGGVANAFSGAFSPITEKDAPALHKLITNMIEDAGDLATRSKDHVYR 120
QY 139 IRPFAFGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPNQONELKRGYELG 196
Db 121 IRPFAFGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELNPNQONELKRGYELG 180
QY 199 QSRVICGYHWQSDVDAARVGSVAVVATLHTNPAFCQQLOKAKAEFAQHKK 249
Db 181 QSRVICGYHWQSDVDAARVGSVAVVATLHTNPAFCQQLOKAKAEFAQHKK 231
RESULT 7
AAW06458

ID XX AAW06458 standard; protein; 248 AA.
AC XX AAW06459;
DT XX 13-AUG-1997 (first entry)
DE XX Enterobacter aerogenes IFO 12010 acid phosphatase.
XX IFO 12010; acid phosphatase; production; nucleoside; 5'-phosphate; ester;
KW condiment; pharmaceutical; intermediate.
XX Enterobacter aerogenes.
OS XX
FH Key Location/Qualifiers
FT Misc-difference 92 /note= "optionally replaced by another amino acid"
FT Misc-difference 171
FT Misc-difference 171 /note= "optionally rep-aced by another amino acid"
XX WO9637603-A1.
PN XX
XX 28-NOV-1996.
PD XX
XX 24-MAY-1996; 96WO-JP001402.
PF XX
XX 25-MAY-1995; 95JP-00149781.
PR XX
XX 26-MAR-1996; 96JP-00094680.
PA (AJIN) AJINOMOTO CO INC.
XX
XX Mihara Y, Utagawa T, Yamada H, Asano Y;
PI WPI; 1997-021215/02.
XX N-PSDB; AAT45007.
DR
XX Efficient production of nucleoside 5'-phosphate - by reaction of a
PT nucleoside with a phosphoric acid donor in the presence of an acid
PT phosphatase.
XX
XX Claim 3; Page 67-68; 95pp; Japanese.
PS
XX The present sequence is the Enterobacter aerogenes IFO 12010 acid
CC phosphate (API), which can be used to produce a nucleoside 5'-phosphate
CC ester from the corresponding nucleoside when a phosphate donor, e.g. poly
CC -, phenyl- or carbamyl-phosphoric acid, is reacted in its presence at pH
CC 3.0 to 5.5. The PA can be used for the economic and efficient production
CC of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals
CC and intermediates for pharmaceuticals
XX
SQ Sequence 248 AA;
Query Match 90.8%; Score 1159; DB 2; Length 248;
Best Local Similarity 90.3%; Pred. No. 6.9e-116;
Matches 224; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
QY 1 MKKRVLCVCPAALFSSQALALVATGNDTTTKPDLYLYLKNSEAINSLALLPPPPAVGSIAP 60
DB 1 MKKRVLCVCPAALFSSQALALVATGNDTTTKPDLYLYLKNSEAINSLALLPPPPAVGSIAP 60
QY 61 LNDQAMYEQGRLLNTERGKLAEDANLSGCVANAFSGAFSPITEKDPALHKLITNM 120
DB 61 LNDQAMYEQGRLLNTERGKLAEDANLSGCVANAFSGAFSPITEKDPALHKLITNM 120
QY 121 IEDAGDLATRSADHYKRIIRPFAPYGVSTCNTTQDKLSKNGSPSGHTSIGWATALVLA 180
DB 121 IEDAGDLATRSADHYKRIIRPFAPYGVSTCNTTQDKLSKNGSPSGHTSIGWATALVLA 180
QY 181 EINFQONEILKRGYELGQSVICGYHWQSDVDAARVVGSAVATLHTNPAFQOOLQAK 240
DB 181 EINFQONEILKRGYELGQSVICGYHWQSDVDAARVVGSAVATLHTNPAFQOOLQAK 240
QY 241 AEFAQHOK 248

Db 241 DEFAKTQK 248
RESULT 8
AAW71031 standard; protein; 248 AA.
ID AAW71031
XX AC AAW71031;
XX 21-OCT-1998 (first entry)
DT XX
DE XX Acid phosphatase enzyme amino acid sequence.
XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
KW intermediate.
XX Enterobacter aerogenes.
OS
XX BP857788-A2.
PN 12-AUG-1998.
PD XX
XX 20-NOV-1997; 97EP-00309365.
PF XX
XX 21-NOV-1996; 96JP-00311103.
PR XX
XX 18-JUN-1997; 97JP-00161674.
XX (AJIN) AJINOMOTO CO INC.
XX Mihara Y, Utagawa T, Yamada H, Asano Y;
PI WPI; 1998-416010/36.
XX N-PSDB; AAV43060.
DR
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT with phosphate donor in presence of acid phosphatase - used as seasonings
PT or pharmaceutical intermediates.
XX
XX Example 23; Page 44; 83pp; English.
PS
XX The present sequence represents an acid phosphatase enzyme. The
CC specification describes a method for the preparation of nucleoside 5'-
CC phosphate esters. The method comprises reacting a nucleoside with a
CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
CC has been altered to increase its affinity for the nucleoside and/or to
CC increase its thermal stability, or in the presence of a microorganism
CC that has been transformed with recombinant DNA containing a gene coding
CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
CC seasonings or pharmaceuticals or as intermediates for them
XX
SQ Sequence 248 AA;
Query Match 90.8%; Score 1159; DB 2; Length 248;
Best Local Similarity 90.3%; Pred. No. 6.9e-116;
Matches 224; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
QY 1 MKKRVLCVCPAALFSSQALALVATGNDTTTKPDLYLYLKNSEAINSLALLPPPPAVGSIAP 60
DB 1 MKKRVLCVCPAALFSSQALALVATGNDTTTKPDLYLYLKNSEAINSLALLPPPPAVGSIAP 60
QY 61 LNDQAMYEQGRLLNTERGKLAEDANLSGCVANAFSGAFSPITEKDPALHKLITNM 120
DB 61 LNDQAMYEQGRLLNTERGKLAEDANLSGCVANAFSGAFSPITEKDPALHKLITNM 120
QY 121 IEDAGDLATRSADHYKRIIRPFAPYGVSTCNTTQDKLSKNGSPSGHTSIGWATALVLA 180
DB 121 IEDAGDLATRSADHYKRIIRPFAPYGVSTCNTTQDKLSKNGSPSGHTSIGWATALVLA 180
QY 181 EINFQONEILKRGYELGQSVICGYHWQSDVDAARVVGSAVATLHTNPAFQOOLQAK 240
DB 181 EINFQONEILKRGYELGQSVICGYHWQSDVDAARVVGSAVATLHTNPAFQOOLQAK 240
QY 241 AEFAQHOK 248

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Db.      241 DEFQKQK 248
||||: ||
RESULT 9
AAW71037
ID AAW71037 standard; protein; 231 AA.
XX
AC AAW71037;
XX
DT 21-OCT-1998 (first entry)
XX
DE Mutant acid phosphatase enzyme of Escherichia blattae.
XX
KW Acid phosphatase; preparation; nuc-eoside 5'-phosphate ester; seasoning;
KW mutant; intermediate.
XX
OS Synthetic.
OS Escherichia blattae.
XX
FH Key Location/Qualifiers
FT Misc-difference 63 /label= L63Q
FT Misc-difference 65 /label= A65Q
FT Misc-difference 66 /label= A65Q
FT Misc-difference 74 /label= E66A
FT Misc-difference 74 /label= G74D
FT Misc-difference 85 /label= S85Y
FT Misc-difference 153 /label= I153T
FT
FT
XX
DN EP857788-A2.
XX
XX 12-AUG-1998.
XX
XX 20-NOV-1997; 97EP-00309365.
XX
XX 21-NOV-1996; 96JP-00311103.
XX 18-JUN-1997; 97JP-00161674.
XX
XX (AJIN ) AJINOMOTO CO INC.
XX
XX Mihara Y, Utagawa T, Yamada H, Asano Y;
XX WPI; 1998-416010/36.
XX
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX with phosphate donor in presence of acid phosphatase - used as seasonings
XX or pharmaceutical intermediates.
XX
XX Example 19; Page; 83pp; English.
XX
XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
XX created using the mature protein of AAW71029. The specification describes
XX a method for the preparation of nucleoside 5'-phosphate esters. The
XX method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
XX 5.5 in the presence of an acid phosphatase that has been altered to
XX increase its affinity for the nucleoside and/or to increase its thermal
XX stability, or in the presence of a microorganism that has been
XX transformed with recombinant DNA containing a gene coding for such an
XX acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
XX pharmaceuticals or as intermediates for them. note: this sequence does
XX not appear in the specification; it was created using information
XX provided
XX
SQ Sequence 231 AA;
Query Match 90.5%; Score 1155; DB 2; Length 231;
Best Local Similarity 97.4%; Pred. No. 1.3e-115;
Matches 225; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 19 LALVATGNDTTTKPDLYLKNSEAINSLALPPPPAVGSIAPNDQAMYQGRLLRNTER 78
|||
Db 1 LALVATGNDTTTKPDLYLKNSEAINSLALPPPPAVGSIAPNDQAMYQGRLLRNTER 60
|||
QY 79 GKLAEDANLSSGGVANAFSGAFGSPITEKDAIPALHKLITNMIEDAGDLATRSKDHVYR 138
|||
Db 61 GKQAQADANLSSGGVANAFSGAFGSPITEKDAIPALHKLITNMIEDAGDLATRSKDHVYR 120
|||
QY 139 IRPFAFVGSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELINPORQNEILKRGVELG 198
|||
Db 121 IRPFAFVGSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLAELINPORQNEILKRGVELG 180
|||
QY 199 QSRVICGYHQSDVDAARVVGSAVVATLHTNPAFQQOLQKAKAFPAHQKK 249
|||
Db 181 QSRVICGYHQSDVDAARVVGSAVVATLHTNPAFQQOLQKAKAFPAHQKK 231
|||
RESULT 10
AAW71038
ID AAW71038 standard; protein; 231 AA.
XX
AC AAW71038;
XX
DT 21-OCT-1998 (first entry)
XX
DE Mutant acid phosphatase enzyme of Escherichia blattae.
XX
KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
KW mutant; intermediate.
XX
OS Synthetic.
OS Escherichia blattae.
XX
FH Key Location/Qualifiers
FT Misc-difference 63 /label= L63Q
FT Misc-difference 65 /label= A65Q
FT Misc-difference 66 /label= A65Q
FT Misc-difference 74 /label= E66A
FT Misc-difference 74 /label= G74D
FT Misc-difference 135 /label= T135K
FT Misc-difference 136 /label= E136D
FT Misc-difference 153 /label= I153T
FT
FT
XX
XX EP857788-A2.
XX
XX 12-AUG-1998.
XX
XX 20-NOV-1997; 97EP-00309365.
XX
XX 21-NOV-1996; 96JP-00311103.
XX 18-JUN-1997; 97JP-00161674.
XX
XX (AJIN ) AJINOMOTO CO INC.
XX
XX Mihara Y, Utagawa T, Yamada H, Asano Y;
XX WPI; 1998-416010/36.
XX
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX with phosphate donor in presence of acid phosphatase - used as seasonings
XX or pharmaceutical intermediates.
XX
XX Example 19; Page; 83pp; English.
XX
XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
XX created using the mature protein of AAW71029. The specification describes
XX a method for the preparation of nucleoside 5'-phosphate esters. The
XX method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
XX 5.5 in the presence of an acid phosphatase that has been altered to
XX increase its affinity for the nucleoside and/or to increase its thermal
XX stability, or in the presence of a microorganism that has been
XX transformed with recombinant DNA containing a gene coding for such an
XX acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
XX pharmaceuticals or as intermediates for them. note: this sequence does
XX not appear in the specification; it was created using information
XX provided
XX
SQ Sequence 231 AA;
Query Match 90.5%; Score 1155; DB 2; Length 231;
Best Local Similarity 97.4%; Pred. No. 1.3e-115;
Matches 225; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

CC a method for the preparation of nucleoside 5'-phosphate esters. The
 CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
 CC 5.5 in the presence of an acid phosphatase that has been altered to
 CC increase its affinity for the nucleoside and/or to increase its thermal
 CC stability, or in the presence of a microorganism that has been
 CC transformed with recombinant DNA containing a gene coding for such an
 CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
 CC pharmaceuticals or as intermediates for them. note: this sequence does
 CC not appear in the specification; it was created using information
 CC provided
 XX
 XX Sequence 231 AA;
 SQ Query Match 90.3%; Score 1152; DB 2; Length 231;
 Best Local Similarity 97.0%; Pred. No. 2.8e-115;
 Matches 224; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 19 LALVATGNDTTTTPDLYLKNSAINSIALPPPPAVGSIAPNDQAMYEQGRLLRNT 78
 Db 1 LALVATGNDTTTTPDLYLKNSAINSIALPPPPAVGSIAPNDQAMYEQGRLLRNT 60
 QY 79 GKLAEDANLSSGVANAFSGARSPITEKDAPALHKLITNMIEDAGLATRSKDHYMR 138
 Db 61 GKQAQADANLSSGVANAFSGARSPITEKDAPALHKLITNMIEDAGLATRSKDHYMR 120
 QY 139 IRPFAEYGVSTCNTTEODKLSKNGSYSPGHTSIGWATLVLAELNPOQNEILKRGYELG 198
 Db 121 IRPFAEYGVSTCNTTEODKLSKNGSYSPGHTSIGWATLVLAELNPOQNEILKRGYELG 180
 QY 199 QSRVICYGVHQSVDVAARVGSVAVVATLHTNPFAFQQOLQKAKAEPAHQKK 249
 Db 181 QSRVICYGVHQSVDVAARVGSVAVVATLHTNPFAFQQOLQKAKAEPAHQKK 231
 RESULT 11
 AAW06459
 ID AAW06459 standard; protein; 248 AA.
 AC AAW06459;
 XX
 XX 17-OCT-2003 (revised)
 DT 13-AUG-1997 (first entry)
 XX
 XX Klebsiella planticola IFO 14939 acid phosphatase.
 XX IFO 14939; acid phosphatase; production; nucleoside; 5'-phosphate; ester;
 KW Condiment; Pharmaceutical; intermediate.
 XX
 XX Racutella planticola.
 XX
 XX Key Location/Qualifiers
 PH Misc-difference 92
 FT Misc-difference /note= "optionally replaced by another amino acid"
 FT Misc-difference 171
 FT Misc-difference /note= "optionally replaced by another amino acid"
 XX
 XX WO9637603-A1.
 EN
 XX 28-NOV-1996.
 PD
 XX 24-MAY-1996; 96WO-JP001402.
 PF
 XX 25-MAY-1995; 95JP-00149781.
 PR 26-MAR-1996; 96JP-00094680.
 XX
 XX (AJIN) AJINOMOTO CO INC.
 PA
 XX Mihara Y, Utogawa T, Yamada H, Asano Y;
 PI
 XX WPI; 1997-021215/02.
 DR N-PSDB; AAY45008.
 XX
 XX Efficient production of nucleoside 5'-phosphate - by reaction of a

PT nucleoside with a phosphoric acid donor in the presence of an acid
 PT phosphatase.
 XX
 XX Claim 3; Page 70-72; 95pp; Japanese.
 PS
 XX The present sequence is the Klebsiella planticola IFO 14939 acid
 CC phosphatase (AP), which can be used to produce a nucleoside 5'-phosphate
 CC ester from the corresponding nucleoside when a phosphate donor, e.g. poly
 CC -, phenyl- or carbamyl-phosphoric acid, is reacted in its presence at pH
 CC 3.0 to 5.5. The PA can be used for the economic and efficient production
 CC of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals
 CC and intermediates for pharmaceuticals. (Updated on 17-OCT-2003 to
 CC standardise OS field)
 XX
 XX Sequence 248 AA;
 SQ Query Match 89.6%; Score 1143; DB 2; Length 248;
 Best Local Similarity 89.1%; Pred. No. 2.9e-114;
 Matches 221; Conservative 12; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MKKRVLAFCFAALFSSQALALVATGNDTTTTPDLYLKNSAINSIALPPPPAVGSIAP 60
 Db 1 MKKRVLAFCFAALFSSQALALVATGNDTTTTPDLYLKNSAINSIALPPPPAVGSIAP 60
 QY 61 LNDQAMYEQGRLLRNTERGKLAEDANLSSGVANAFSGARSPITEKDAPALHKLITNM 120
 Db 61 LNDQAMYEQGRLLRNTERGKLAEDANLSSGVANAFSGARSPITEKDAPALHKLITNM 120
 QY 121 IEDAGLATRSKDHYMRIRPFAEYGVSTCNTTEODKLSKNGSYSPGHTSIGWATLVLA 180
 Db 121 IEDAGLATRSKDHYMRIRPFAEYGVSTCNTTEODKLSKNGSYSPGHTSIGWATLVLA 180
 QY 181 EINPORQNEILKRGYELGQSRVICGYHWSVDVAARVGSVAVVATLHTNPFAFQQOLQKAK 240
 Db 181 EINPORQNEILKRGYELGQSRVICGYHWSVDVAARVGSVAVVATLHTNPFAFQQOLQKAK 240
 QY 241 AEPAHQKK 248
 Db 241 DEFAHQKK 248
 RESULT 12
 AAW71032
 ID AAW71032 standard; protein; 248 AA.
 AC AAW71032;
 XX 27-AUG-2003 (revised)
 DT 21-OCT-1998 (first entry)
 XX
 XX Acid phosphatase enzyme amino acid sequence.
 DE
 XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 KW intermediate.
 XX
 XX Racutella planticola.
 OS
 XX EP857788-A2.
 PN
 XX 12-AUG-1998.
 PD
 XX 20-NOV-1997; 97EP-00309365.
 PF
 XX 21-NOV-1996; 96JP-00311103.
 PR 18-JUN-1997; 97JP-00161674.
 XX
 XX (AJIN) AJINOMOTO CO INC.
 PA
 XX Mihara Y, Utogawa T, Yamada H, Asano Y;
 PI
 XX WPI; 1998-416010/36.
 DR N-PSDB; AAV43061.
 XX
 XX

PT Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 PT with phosphate donor in presence of acid phosphatase - used as seasonings
 PT or pharmaceutical intermediates.

XX Claim 6; Page 46-47; 83pp; English.

XX The present sequence represents an acid phosphatase enzyme. The
 CC specification describes a method for the preparation of nucleoside 5'-
 CC phosphate esters. The method comprises reacting a nucleoside with a
 CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
 CC has been altered to increase its affinity for the nucleoside and/or to
 CC increase its thermal stability, or in the presence of a microorganism
 CC that has been transformed with recombinant DNA containing a gene coding
 CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
 CC seasonings or pharmaceuticals or as intermediates for them. note: this
 CC sequence appears as SEQ ID number 25 (nucleic acid) in the claims, but it
 CC is clear that the protein is being claimed. (Updated on 27-AUG-2003 to
 CC correct OS field.)

XX SQ Sequence 248 AA;

Query Match 89.6%; Score 1143; DB 2; Length 248;
 Best Local Similarity 89.1%; Pred. No. 2.9e-114;
 Matches 221; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 MKKRVLAVCFPAALFSSQALALVATGNDTTKPDLYLKNSEAINSLALLPPPPAVGSI 60
 DB 1 MKKRVLALCLASFVSAFALVPAGNDATTKPDLYLKNQAIDSLALLPPPEVGSIAF 60
 QY 61 LNDQAMYEQGRLLRNTERGKLAEDANLSGGVANAFSGAFSPITEKDAPALHKLITNM 120
 DB 61 LNDQAMYEKGRLLRNTARGKLAEDANLSAGGVANAFSAAFSGPISEKDAPALHKLITNM 120
 QY 121 IEDAGLATRSKDHVMRIIPFAYGVSTCNTTEODKLSKNGSVPSGHTSIGWATLVLA 180
 DB 121 IEDAGLATRGAKYKRIIPFAYGVSTCNTTEODKLSKNGSVPSGHTSIGWATLVLA 180
 QY 181 EIPQRCNEILKRGYELGQSRVIGYHWSQSDVDAAVVGVSAVATLHTNPAFQOOLQKAK 240
 DB 181 EIPQRCNEILKRGYELGESRVIGYHWSQSDVDAAIRVGSVAVATLHTNPAFQOOLQKAK 240
 QY 241 AEFAHQK 248
 DB 241 DEFAKQK 248

RESULT 13

AAW71039
 ID AAW71039 standard; protein; 231 AA.

XX AAW71039;

XX 21-OCT-1998 (first entry)

XX Mutant acid phosphatase enzyme of Escherichia blattae.

XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 KW mutant; intermediate.

XX Synthetic.

OS Escherichia blattae.

XX Key Location/Qualifiers

FT MISC-difference 63 /label= L63Q

FT MISC-difference 65 /label= A65Q

FT MISC-difference 66 /label= E66A

FT MISC-difference 69 /label= N69D

FT MISC-difference 71 /label= S71A

FT MISC-difference 72 /label= S72A
 FT MISC-difference 74 /label= G74D
 FT MISC-difference 135 /label= T135K
 FT MISC-difference 136 /label= E136D
 FT MISC-difference 153 /label= I153T
 XX

PN EP857788-A2.

XX 12-AUG-1998.

XX 20-NOV-1997; 97EP-00309365.

XX 21-NOV-1996; 96JP-00311103.

XX 18-JUN-1997; 97JP-00161674.

XX (AJIN) AJINOMOTO CO INC.

XX Mihara Y, Utagawa T, Yamada H, Asano Y;

XX WPI; 1998-416010/36.

XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 PT with phosphate donor in presence of acid phosphatase - used as seasonings
 PT or pharmaceutical intermediates.

XX Example 19; Page; 83pp; English.

XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
 CC created using the mature protein of AAW71029. The specification describes
 CC a method for the preparation of nucleoside 5'-phosphate esters. The
 CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
 CC 5.5 in the presence of an acid phosphatase that has been altered to
 CC increase its affinity for the nucleoside and/or to increase its thermal
 CC stability, or in the presence of a microorganism that has been
 CC transformed with recombinant DNA containing a gene coding for such an
 CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
 CC pharmaceuticals or as intermediates for them. note: this sequence does
 CC not appear in the specification; it was created using information
 CC provided

XX SQ Sequence 231 AA;

Query Match 89.4%; Score 1141; DB 2; Length 231;

Best Local Similarity 95.7%; Pred. No. 4.2e-114;

Matches 221; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 19 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAPLNDQAMYEQGRLLRNT 78

DB 1 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAPLNDQAMYEQGRLLRNT 60

QY 79 GKLAEDANLSSGGVANAFSGAFSPITEKDAPALHKLITNMIEDAGLATRSKDHVMR 138

DB 61 GKQAQADADLAAGSVANAFSGAFSPITEKDAPALHKLITNMIEDAGLATRSKDHVMR 120

QY 139 IRPFAYGVSTCNTTEODKLSKNGSVPSGHTSIGWATLVLAEPQNEILKRGYELG 198

DB 121 IRPFAYGVSTCNTTEODKLSKNGSVPSGHTSIGWATLVLAEPQNEILKRGYELG 180

QY 199 QSRVICGYHWSQSDVDAAVVGVSAVATLHTNPAFQOOLQKAKAEFAHQK 249

DB 181 QSRVICGYHWSQSDVDAAVVGVSAVATLHTNPAFQOOLQKAKAEFAHQK 231

RESULT 14

AAW71040

ID AAW71040 standard; protein; 231 AA.

XX AAW71040;

XX 21-OCT-1998 (first entry)
 XX Mutant acid phosphatase enzyme of Escherichia biattae.
 DE Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 XX mutant; intermediate.
 XX Synthetic.
 OS Escherichia biattae.
 XX Key Location/Qualifiers
 PH Misc-difference 63 /label= L63Q
 FT Misc-difference 65 /label= A65Q
 FT Misc-difference 66 /label= E66A
 FT Misc-difference 69 /label= M69D
 FT Misc-difference 71 /label= S71A
 FT Misc-difference 72 /label= S72A
 FT Misc-difference 74 /label= G74D
 FT Misc-difference 116 /label= D116E
 FT Misc-difference 135 /label= T135K
 FT Misc-difference 136 /label= E136D
 FT Misc-difference 153 /label= I153T
 FT
 XX EP857788-A2.
 PN 12-AUG-1998.
 PD 20-NOV-1997; 97EP-00309365.
 PP 21-NOV-1996; 96JP-00311103.
 PR 18-JUN-1997; 97JP-00161674.
 XX (AJIN) AJINOMOTO CO INC.
 PA Mihara Y, Utagawa T, Yamada H, Asano Y;
 PI MPI; 1998-416010/36.
 XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 XX with phosphate donor in presence of acid phosphatase - used as seasonings
 XX or pharmaceutical intermediates.
 XX Example 19; Page; 83pp; English.
 PS
 XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
 CC created using the mature protein of AAW71029. The specification describes
 CC a method for the preparation of nucleoside 5'-phosphate esters. The
 CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
 CC 5.5 in the presence of an acid phosphatase that has been altered to
 CC increase its affinity for the nucleoside and/or to increase its thermal
 CC stability, or in the presence of a microorganism that has been
 CC transformed with recombinant DNA containing a gene coding for such an
 CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
 CC pharmaceuticals or as intermediates for them. note: this sequence does
 CC not appear in the specification; it was created using information
 CC provided
 XX Sequence 231 AA;

Query Match 89.1%; Score 1137; DB 2; Length 231;
 Best Local Similarity 95.2%; Pred. No. 1,1e-113;

Matches 220; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 19 LALVATGNDTTTTPDLYLKNSEAINSLALLPPPPAVGSIATLNDQAMYGQRLRNTER 78
 DB 1 LALVATGNDTTTTPDLYLKNSEAINSLALLPPPPAVGSIATLNDQAMYGQRLRNTER 60
 QY 79 GKLAEDANLSSGGVANAFSGAFGSPITKXDAALHKLTLNMIEDAGDLATRSKDHMYR 138
 DB 61 GKQQAQADADLAAGDVANAFSGAFGSPITKXDAALHKLTLNMIEDAGDLATRSKDHMYR 120
 QY 139 IRPFAYGVSTCNTTQDKLSKNGSYPSGHTSGTATALVLAEPORONEILKRGVELG 198
 DB 121 IRPFAYGVSTCNTTQDKLSKNGSYPSGHTSGTATALVLAEPORONEILKRGVELG 180
 QY 199 QSRVICGYHWCSDVDAARVVGSVAVATLHTNPAFQQQLQKAKAEFAHQKK 249
 DB 181 QSRVICGYHWCSDVDAARVVGSVAVATLHTNPAFQQQLQKAKAEFAHQKK 231
 RESULT 15
 AAW71041
 ID AAW71041 standard; protein; 231 AA.
 XX
 AC AAW71041;
 XX
 DT 21-OCT-1998 (first entry)
 XX
 DE Mutant acid phosphatase enzyme of Escherichia biattae.
 XX
 KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 KW mutant; intermediate.
 XX
 OS Synthetic.
 OS Escherichia biattae.
 XX Key Location/Qualifiers
 FH Misc-difference 63 /label= L63Q
 FT Misc-difference 65 /label= A65Q
 FT Misc-difference 66 /label= E66A
 FT Misc-difference 69 /label= M69D
 FT Misc-difference 71 /label= S71A
 FT Misc-difference 72 /label= S72A
 FT Misc-difference 74 /label= G74D
 FT Misc-difference 116 /label= D116E
 FT Misc-difference 130 /label= S130E
 FT Misc-difference 135 /label= T135K
 FT Misc-difference 136 /label= E136D
 FT Misc-difference 153 /label= I153T
 XX
 PN EP857788-A2.
 XX 12-AUG-1998.
 XX 20-NOV-1997; 97EP-00309365.
 XX 21-NOV-1996; 96JP-00311103.
 PR 18-JUN-1997; 97JP-00161674.
 XX (AJIN) AJINOMOTO CO INC.
 PA Mihara Y, Utagawa T, Yamada H, Asano Y;

XX WEI; 1998-416010/36.
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT with phosphate donor in presence of acid phosphatase - used as seasonings
PT or pharmaceutical intermediates.
XX
XX Example 19; Page; 83pp; English.
XX
XX AAW71034-42 represent mutant acid phosphatase enzymes. The mutants were
CC created using the mature protein of AAW71029. The specification describes
CC a method for the preparation of nucleoside 5'-phosphate esters. The
CC method comprises reacting a nucleoside with a phosphate donor at pH 3.0-
CC 5.5 in the presence of an acid phosphatase that has been altered to
CC increase its affinity for the nucleoside and/or to increase its thermal
CC stability, or in the presence of a microorganism that has been
CC transformed with recombinant DNA containing a gene coding for such an
CC acid phosphatase. Nucleoside 5'-phosphates are useful as seasonings or
CC pharmaceuticals or as intermediates for them. note: this sequence does
CC not appear in the specification; it was created using information
CC provided
XX
XX Sequence 231 AA;

Query Match 88.8%; Score 1133; DB 2; Length 231;
Best Local Similarity 94.8%; Pred. No. 3.1e-113;
Matches 219; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 19 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPAVGSFAPLNDQAMYEQGRLLRTER 78
Db 1 LALVATGNDTTTKPDLYLKNSEAINSLALLPPPAVGSFAPLNDQAMYEQGRLLRTER 60
QY 79 GKLAEDANLSGGVANAFSGAFSPITEKAPALHKLTLNMIEDAGDLATRSKOHYMR 138
Db 61 GKQAQADADLAGDVANAFSGAFSPITEKAPALHKLTLNMIEDAGDLATRSKOHYMR 120
QY 139 IRPFAFYGVSTCNTTEQDKLSKNGSVPSGHTSIGWATLVLAEINPQRQNEILKRGYELG 198
Db 121 IRPFAFYGVETCNTKQDKLSKNGSVPSGHTSIGWATLVLAEINPQRQNEILKRGYELG 180
QY 199 QSRVICGYHWQSDVDAARVVGSAVATLHTNPAPFOOLQKAKAEFAHQKK 249
Db 181 QSRVICGYHWQSDVDAARVVGSAVATLHTNPAPFOOLQKAKAEFAHQKK 231

Search completed: June 2, 2004, 10:45:27
Job time : 63 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2004, 10:42:44 ; Search time 46 seconds
(without alignments)
1707.914 Million cell updates/sec

Title: US-09-807-990-2

Perfect score: 1276

Sequence: 1 MKKRVLAVCPAALFSSQALA.....PAFQQLOKAKFAHQKK 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315519202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.podent:*
- 12: sp.virus:*
- 13: sp.vertebrate:*
- 14: sp.unclassified:*
- 15: sp.rvirus:*
- 16: sp.bacteriap:*
- 17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1276	133.0	249	2	Q9S1A6	Q9S1A6 escherichia
2	1158	93.8	248	2	Q9F1U1	Q9F1U1 enterobacte
3	1143	89.6	248	2	Q9F1U0	Q9F1U0 klebsiella
4	1124	88.1	248	2	Q9RLW6	Q9RLW6 klebsiella
5	1048	82.1	249	2	Q50542	Q50542 shigella fl
6	1044	81.8	249	2	Q99Q99	Q99Q99 shigella fl
7	789	61.8	263	2	Q87188	Q87188 prevotella
8	596	46.7	246	2	Q99Q95	Q99Q95 shigella fl
9	591	46.3	246	2	Q99Q99	Q99Q99 shigella fl
10	590	46.2	246	2	Q931G8	Q931G8 escherichia
11	478	37.5	250	2	Q8KRUE	Q8KRUE salmonella
12	474.5	37.2	285	16	Q8PEI0	Q8PEI0 xanthomonas
13	433.5	34.0	280	16	Q8P342	Q8P342 xanthomonas
14	418.5	32.8	289	16	Q7TUQ8	Q7TUQ8 prochloroco
15	274.5	21.5	258	16	Q9AB73	Q9AB73 caulobacter
16	221	17.3	231	16	Q98HU7	Q98HU7 rhizobium 1

17 190 14.9 423 16 Q8ZLDS
18 189.5 14.9 2314 16 Q69822
19 175.5 13.8 241 16 Q916U4
20 167 13.1 591 16 Q97L24
21 149 11.7 986 16 Q87U02
22 144.5 11.3 128 16 Q7TU07
23 144.5 11.3 657 16 Q8Y350
24 143 11.2 622 16 Q8NR65
25 141 11.1 660 16 Q8U788
26 130.5 10.2 513 16 Q8G856
27 115 9.0 260 16 Q8E929
28 106.5 8.3 201 17 Q8TW45
29 105 8.2 145 16 Q9RVL3
30 103.5 8.1 178 16 Q8R7A7
31 103 8.1 1381 17 Q8TRM0
32 101.5 8.0 266 16 Q89CT4
33 100 7.8 230 16 Q9K3L3
34 99.5 7.8 151 16 Q8KFG2
35 99.5 7.8 259 16 Q9A424
36 99.5 7.8 353 10 Q84R60
37 97.5 7.6 487 2 P72269
38 96 7.5 178 16 Q9KP85
39 96 7.5 824 16 Q83SL8
40 95.5 7.5 235 16 Q92KY7
41 95.5 7.5 307 16 Q8FLZ6
42 95 7.4 320 16 Q8YWA0
43 95 7.4 451 16 Q8G0H4
44 94 7.4 824 16 Q8X904
45 94 7.4 1321 16 Q8PR59

ALIGNMENTS

RESULT 1

Q9S1A6 PRELIMINARY; PRT; 249 AA.
ID Q9S1A6;
AC Q9S1A6;
DC 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Acid phosphatase (EC 3.1.3.2).
GN PHO.
OS Escherichia blattae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=563;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM1650;
RX MEDLINE=20296667; PubMed=10835340;
RA Ishikawa K., Mihara Y., Gondoh K., Suzuki E., Asano Y.;
RT "X-ray structures of a novel acid phosphatase from Escherichia blattae
RT and its complex with the transition-state analog molybdate.";
RL EMBO J. 19:2412-2423 (2000).
DR EMBL; AB020481; BAB84942.1; .
DR PDB; 1D2T; 06-DEC-00.
DR PDB; 1E01; 23-MAR-01.
DR PDB; 1TW8; 11-SEP-02.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR008934; AcPase Vanperase.
DR InterPro; IPR001011; Bac AcPaseA.
DR InterPro; IPR000326; PA_PTPase.
DR Pfam; PF01569; PAP2; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac AcPaseA; 1.
DR SMART; SM00014; acidPPC; 1.
DR PROSITE; PS01157; ACID_PHOSPH_CL_A; 1.
KW Hydrolase.
SEQUENCE 249 AA; 26956 MW; 7A8AE6CB1FC0CA3 CRC64;

Q8ZLDS salmonella
Q69822 streptomyce
Q916U4 pseudomonas
Q97L24 clostridium
Q87U02 pseudomonas
Q7TUJ7 prochloroco
Q8Y350 ralistonia s
Q8NR65 corynebacte
Q8U788 agrobacteri
Q8G856 bifidobacte
Q8E929 shewanella
Q8TW45 methanopyru
Q9RVL3 deinococcus
Q8R7A7 thermoaer
Q8TRM0 methanosarc
Q89CT4 bradyrhizob
Q9K3L3 streptomyce
Q8KFG2 chlorobium
Q9A424 caulobacter
Q84R60 oryza sativ
P72269 rhodococcus
Q9KP85 vibrio chol
Q83SL8 shigella fl
Q92KY7 rhizobium m
Q8FLZ6 corynebacte
Q8YWA0 anabaena sp
Q8G0H4 bruceella su
Q8X904 escherichia
Q8PR59 xanthomonas

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Query Match      100.0%; Score 1276; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 4.8e-103;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKKRVAVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAP 60
DB 1 MKKRVAVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAP 60

QY 61 LNDQMYEGGRLLRNTERGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 120
DB 61 LNDQMYEGGRLLRNTERGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 120

QY 121 IEDAGDLATRSADHYMRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLA 180
DB 121 IEDAGDLATRSADHYMRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLA 180

QY 181 EINPQRONEILKRGYELGQSRVICGYHMQSDVDAARVGVSAVATLHTNPAFQOOLQKAK 240
DB 181 EINPQRONEILKRGYELGQSRVICGYHMQSDVDAARVGVSAVATLHTNPAFQOOLQKAK 240

QY 241 AEFQHQK 249
DB 241 AEFQHQK 249

RESULT 2
Q9F1U1 PRELIMINARY; PRT; 248 AA.
ID Q9F1U1
AC Q9F1U1
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE ACID phosphatase.
GN PHO.
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=548;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO12010;
RA Mihara Y., Utagawa T., Matsui H., Asano Y.;
RT "Acid phosphatase/phosphotransferase from enteric bacteria.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB044338; BAB18917.1; -.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000934; A:AcPase VanPerase.
DR InterPro; IPR001011; B:Ac AcPaseA.
DR InterPro; IPR00326; P:ATPase.
DR Pfam; PF01569; PAP2; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac AcPaseA; 1.
DR SMART; SM00014; acdPPC; 1.
DR PROSITE; PS01157; ACID_PHOSP CL_A; 1.
SQ SEQUENCE 248 AA; 26963 MW; 208FAC2E5EB62D CRC64;

Query Match      90.8%; Score 1158; DB 2; Length 248;
Best Local Similarity 90.3%; Pred. No. 9.1e-93;
Matches 224; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKKRVAVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAP 60
DB 1 MKKRVAVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAP 60

QY 61 LNDQMYEGGRLLRNTERGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 120
DB 61 LNDQMYEGGRLLRNTERGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 120

QY 121 IEDAGDLATRSADHYMRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLA 180
DB 121 IEDAGDLATRSADHYMRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLA 180

QY 181 EINPQRONEILKRGYELGQSRVICGYHMQSDVDAARVGVSAVATLHTNPAFQOOLQKAK 240
DB 181 EINPQRONEILKRGYELGQSRVICGYHMQSDVDAARVGVSAVATLHTNPAFQOOLQKAK 240

QY 241 AEFQHQK 249
DB 241 AEFQHQK 249

RESULT 4
Q9RLW6 PRELIMINARY; PRT; 248 AA.
ID Q9RLW6
AC Q9RLW6
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

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QY 181 EINPQRONEILKRGYELGQSRVICGYHMQSDVDAARVGVSAVATLHTNPAFQOOLQKAK 240
DB 181 EINPQRONEILKRGYELGQSRVICGYHMQSDVDAARVGVSAVATLHTNPAFQOOLQKAK 240

QY 241 AEFQHQK 248
DB 241 DEFQHQK 248

RESULT 3
Q9FIU0 PRELIMINARY; PRT; 248 AA.
ID Q9FIU0
AC Q9FIU0
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE ACID phosphatase.
GN PHO.
OS Klebsiella planticola (Raoultella planticola).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Raoultella.
OX NCBI_TaxID=575;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO14939;
RA Mihara Y., Utagawa T., Matsui H., Asano Y.;
RT "Acid phosphatase/phosphotransferase from enteric bacteria.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB044345; BAB18918.1; -.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000934; A:AcPase VanPerase.
DR InterPro; IPR001011; B:Ac AcPaseA.
DR InterPro; IPR00326; P:ATPase.
DR Pfam; PF01569; PAP2; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac AcPaseA; 1.
DR SMART; SM00014; acdPPC; 1.
DR PROSITE; PS01157; ACID_PHOSP CL_A; 1.
SQ SEQUENCE 248 AA; 26745 MW; 68F65CA2448EB3EF CRC64;

Query Match      89.6%; Score 1143; DB 2; Length 248;
Best Local Similarity 89.1%; Pred. No. 1.9e-91;
Matches 221; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 MKKRVAVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAP 60
DB 1 MKKRVAVCFALFSSQALALVATGNDTTTKPDLYLKNSEAINSLALLPPPPAVGSIAP 60

QY 61 LNDQMYEGGRLLRNTERGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 120
DB 61 LNDQMYEGGRLLRNTERGKLAEDANLSSGGVANAFSGAFSPITEKDA PALHKLITNM 120

QY 121 IEDAGDLATRSADHYMRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLA 180
DB 121 IEDAGDLATRSADHYMRIRPFAYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATLVLA 180

QY 181 EINPQRONEILKRGYELGQSRVICGYHMQSDVDAARVGVSAVATLHTNPAFQOOLQKAK 240
DB 181 EINPQRONEILKRGYELGQSRVICGYHMQSDVDAARVGVSAVATLHTNPAFQOOLQKAK 240

QY 241 AEFQHQK 248
DB 241 DEFQHQK 248

RESULT 4
Q9RLW6 PRELIMINARY; PRT; 248 AA.
ID Q9RLW6
AC Q9RLW6
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

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DE Phoc protein precursor (EC 3.1.1.3.2).
GN PHOC.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]_SEQUENCE FROM N.A.
RP STRAIN=CCUG 225;
RC Passariello C., Berlutti F., Selan L., Thaller M.C., Rossolini G.;
RA "Klebsiella pneumoniae Phoc: a new member of the class A1 bacterial
RT acid phosphatases family";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ250377; CAB59725.1; -.
DR GO: 00030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO: 0003993; F:acid phosphatase activity; IEA.
DR GO: 0016787; F:hydrolase activity; IEA.
DR InterPro: IPR008934; ACPase VanPerase.
DR InterPro: IPR001011; Bac AcPaseA.
DR Pfam: PF01569; PAP2; 1.
DR PRINTS: PR00483; BACPHPTASE.
DR ProDom: PD009838; Bac AcPaseA; 1.
DR SMART: SM00014; acidPPC; 1.
DR PROSITE: PS01157; ACID_PHOSPH_CL_A; 1.
KW Hydrolase; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 248 PHOC.
SQ SEQUENCE 248 AA; 27110 MW; ED6E9D8663636B0D CRC64;

Query Match 88.1%; Score 1124; DB 2; Length 248;
Best Local Similarity 87.5%; Pred. No. 8.4e-90;
Matches 217; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 MKKRLVAVCFPAALFSSQALALVATGNDTTTKPDLYYLKNSAINSALLPPPPAVGSIAP 60
DB 1 MKKRLVAVCFPAALFSSQALALVATGNDTTTKPDLYYLKNSAINSALLPPPPAVGSIAP 60

QY 61 LNDQMYEQGLLNTNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAALHKLNTNM 120
DB 61 LNDQMYEQGLLNTNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAALHKLNTNM 120

QY 121 IEDAGDLATRSADHYMRIRPFYFVSTGNTTQDKLKNGSVPSGHTSIGWATALVLA 180
DB 121 IEDAGDLATRSADHYMRIRPFYFVSTGNTTQDKLKNGSVPSGHTSIGWATALVLA 180

QY 181 EINFQONEILKRGYELGQSRVIGYHWQSDVDAAARVGVSAVATLTNPAFOOQLOKAK 240
DB 181 EINFQONEILKRGYELGQSRVIGYHWQSDVDAAARVGVSAVATLTNPAFOOQLOKAK 240

QY 241 AEFAHQK 248
DB 241 DEFAKQK 248

RESULT 5
ID OS0542 PRELIMINARY; PRT; 249 AA.
AC OS0542;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nonspecific phosphatase.
GN PHOC.
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YSH6000;
RC MEDLINE=96345620; PubMed=8755883;
RX

RA Uchiya K., Toheuji M., Nikai T., Sugihara H., Sasaki C.;
RT "Identification and characterization of phoN-Sf, a gene on the large
RL plasmid of Shigella flexneri 2a encoding a nonspecific phosphatase";
J. Bacteriol. 178:4548-4554(1996).
DR EMBL: D82966; EAA11655.1; -.
DR GO: 0046821; C:extrachromosomal DNA; IEA.
DR GO: 00030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO: 0003993; F:acid phosphatase activity; IEA.
DR InterPro: IPR008934; ACPase VanPerase.
DR InterPro: IPR001011; Bac AcPaseA.
DR InterPro: IPR000326; PA_FTPase.
DR Pfam: PF01569; PAP2; 1.
DR PRINTS: PR00483; BACPHPTASE.
DR ProDom: PD009838; Bac AcPaseA; 1.
DR SMART: SM00014; acidPPC; 1.
DR PROSITE: PS01157; ACID_PHOSPH_CL_A; 1.
KW Plasmid.
SQ SEQUENCE 249 AA; 27177 MW; 58F34CEB034EE070 CRC64;

Query Match 82.1%; Score 1048; DB 2; Length 249;
Best Local Similarity 79.9%; Pred. No. 3.5e-83;
Matches 199; Conservative 19; Mismatches 31; Indels 0; Gaps 0;

QY 1 MKKRLVAVCFPAALFSSQALALVATGNDTTTKPDLYYLKNSAINSALLPPPPAVGSIAP 60
DB 1 MKKRLVAVCFPAALFSSQALALVATGNDTTTKPDLYYLKNSAINSALLPPPPAVGSIAP 60

QY 61 LNDQMYEQGLLNTNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAALHKLNTNM 120
DB 61 LNDQMYEQGLLNTNTERGKLAEDANLSSGGVANAFSGAFSPITEKDAALHKLNTNM 120

QY 121 IEDAGDLATRSADHYMRIRPFYFVSTGNTTQDKLKNGSVPSGHTSIGWATALVLA 180
DB 121 IEDAGDLATRSADHYMRIRPFYFVSTGNTTQDKLKNGSVPSGHTSIGWATALVLA 180

QY 181 EINFQONEILKRGYELGQSRVIGYHWQSDVDAAARVGVSAVATLTNPAFOOQLOKAK 240
DB 181 EINFQONEILKRGYELGQSRVIGYHWQSDVDAAARVGVSAVATLTNPAFOOQLOKAK 240

QY 241 AEFAHQK 249
DB 241 DEFAHQK 249

RESULT 6
ID Q99Q99 PRELIMINARY; PRT; 249 AA.
AC Q99Q99;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phon1, periplasmic non specific acid oisophatase (Phoshatase
DE precursor)
GN PHON1 OR PHON-SF.
OS Shigella flexneri, and
OS Shigella flexneri 2a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623, 42897;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=M90T;
RC MEDLINE=20566792; PubMed=1115111;
RA Buchrieser C., Glaser P., Rumnok C.,
RA Kunst F., Sansonetti P., Parsot C.;
RT "The virulence plasmid pWR100 and the repertoire of proteins secreted
RL by the type III secretion apparatus of Shigella flexneri";
Mol. Microbiol. 38:760-771(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; PLASMID=virulence pWR501;
RA Venkatesan M.M., Goldberg M.B., Rose D.J., Grotbeck E.J., Burland V.,
RA Blattner F.R.;


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RT Shigella flexneri.;
RL Infect. Immun. 0:0-0(2001).
DR EMBL; AL391753; CACO5771.1; -.
DR EMBL; AF348706; AAK18315.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR008934; AcPase VanPerase.
DR InterPro; IPR001011; Bac AcPaseA.
DR InterPro; IPR000326; PA_PTPase.
DR Pfam; PF01569; PAP2; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac AcPaseA; 1.
DR SMART; SM00014; acidPPC; 1.
KW Plasmid.
SQ SEQUENCE 246 AA; 27559 MW; 48D76BD8CC7885E5 CRC64;

Query Match 46.7%; Score 596; DB 2; Length 246;
Best Local Similarity 48.6%; Pred. No. 8.6e-44;
Matches 119; Conservative 44; Mismatches 69; Indels 14; Gaps 3;

QY 3 KRVLAVCFAA--LFSSQALALVATGNDTTTPDLYLKNSEAINSLALLPPPPAVGSIATF 60
DB 4 KNFLFCIATNMIFIPSANALKAEG-----FLTQQTSPDLSILPPPPAENSVPF 53

QY 61 LNDQAMYEQGRLLRNTGRKLAEDANLSSGGVANAFSGAFSPITEKDPALHKLITNM 120
DB 54 LADKAHYEFGSLRDANVRVLAEDAYYENFGL--AFSDAYGMDISRENTPIYLQITQV 111

QY 121 IEDAGDLATRSADKHYMRIRPFAPYGVSTQNTTEODKLSKNGSPSGHTSIGWATALVIA 180
DB 112 LQSDHDAVRAKAYKVRPFVIYKDATCTPDKDKMAITGSPSGHAFGMAVALILA 171

QY 181 EINPQRQNEILLKRGVEYLGQSRIVCYHMQSDVDAARVVGSAVATLHTNPAFOOQLOKAK 240
DB 172 EINPQRKAEILLRGGYFEGESRIVCGAHWQSDVEAGRLMGASVVAVLHNTPEFTKLSLSEAK 231

QY 241 AEPAQ 245
DB 232 KEFEE 236

RESULT 5
Q59909
ID Q59909 PRELIMINARY; PRT; 246 AA.
AC Q59909;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ATP diphosphohydrolase, apyrase precursor (BC 3.6.1.5).
GN Apy.
OS Shigella flexneri, and
OS Shigella flexneri 2a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623, 42897;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=2a;
RA Ramchandran V., Sankaran K., Subrahmanyam Y.V.B.K., Ramakrishnan R.,
RA Datta S., Roy R.K.;
RT "Virulent Shigella codes for a soluble apyrase : Identification,
RT characterisation and cloning of the gene";
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri 2a; STRAIN=301; PLASMID=PCP301;
RA Jin Q., Zhang J.Y., Liu H., Yang J., Yang F., Zhang X.B., Wang J.H.,
RA Yang G.W., Wu H.T., Dong J., Sun L.L., Xue Y., Zhao A.L., Gao Y.S.,
RA Zhu J.P., Kan B., Chen S.X., Yao Z.J., He B.K., Chen R.S., Ma D.L.,
RA Yuan Z.H., Xu J.G., Wang Y., Shen Y., Lu W.C., Qiang B.Q., Wen Y.M.,
RA Hou Y.D.;
RT "Complete DNA sequence and analysis of the large virulence plasmid

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RT pCP301 of Shigella flexneri.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U04539; AAA21206.1; -.
DR EMBL; AF386526; AAL72358.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR GO; GO:0004050; F:apyrase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR008934; AcPase VanPerase.
DR InterPro; IPR001011; Bac AcPaseA.
DR InterPro; IPR000326; PA_PTPase.
DR Pfam; PF01569; PAP2; 1.
DR PRINTS; PR00483; BACPHPTASE.
DR ProDom; PD009838; Bac AcPaseA; 1.
DR SMART; SM00014; acidPPC; 1.
KW Hydrolase; Signal; Plasmid.
FT SIGNAL 1 23
SQ SEQUENCE 246 AA; 27573 MW; B81737D9B6143912 CRC64;

Query Match 46.3%; Score 591; DB 2; Length 246;
Best Local Similarity 48.2%; Pred. No. 2.3e-43;
Matches 118; Conservative 44; Mismatches 69; Indels 14; Gaps 3;

QY 3 KRVLAVCFAA--LFSSQALALVATGNDTTTPDLYLKNSEAINSLALLPPPPAVGSIATF 60
DB 4 KNFLFCIATNMIFIPSANALKAEG-----FLTQQTSPDLSILPPPPAENSVPF 53

QY 61 LNDQAMYEQGRLLRNTGRKLAEDANLSSGGVANAFSGAFSPITEKDPALHKLITNM 120
DB 54 QADKAHYEFGSLRDANVRVLAEDAYYENFGL--AFSDAYGMDISRENTPIYLQITQV 111

QY 121 IEDAGDLATRSADKHYMRIRPFAPYGVSTQNTTEODKLSKNGSPSGHTSIGWATALVIA 180
DB 112 LQSDHDAVRAKAYKVRPFVIYKDATCTPDKDKMAITGSPSGHAFGMAVALILA 171

QY 181 EINPQRQNEILLKRGVEYLGQSRIVCYHMQSDVDAARVVGSAVATLHTNPAFOOQLOKAK 240
DB 172 EINPQRKAEILLRGGYFEGESRIVCGAHWQSDVEAGRLMGASVVAVLHNTPEFTKLSLSEAK 231

QY 241 AEPAQ 245
DB 232 KEFEE 236

RESULT 10
Q93IG8
ID Q93IG8 PRELIMINARY; PRT; 246 AA.
AC Q93IG8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Apyrase (BC 3.6.1.5).
GN Apy.
OS Escherichia coli.
OS Plasmid pHN280.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Santapaula D., Casalino M., Petrucci A., Presutti C., Zagaglia C.,
RA Berlutti F., Colonna B., Nicoletti M.;
RT "Virulence plasmid-carried apyrase gene (apy) is cotranscribed with the
RT upstream ospB gene in enteroinvasive Escherichia coli: study of
RT transcriptional organization and regulation of the ospB-apy operon.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RL EMBL; AJ315184; CAC67470.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR GO; GO:0004050; F:apyrase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.

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DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Acid phosphatase.
GN CC0358.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
CX NCBI_TaxID=155892;
RN [-]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Mierman W.C.; Feldblyum T.V.; Laub M.T.; Paulsen I.T.; Nelson K.E.;
RA Eisen J.; Heidelberg J.F.; Alley M.R.K.; Ohta N.; Maddock J.R.; Ely B.;
RA Petocka I.; Nelson W.C.; Newton A.; Stephens C.; Shadke N.D.; Ely B.;
RA DeBoy R.T.; Dodson R.J.; Durkin A.S.; Gwinn M.L.; Haft D.H.;
RA Kolonay J.F.; Smit J.; Craven M.B.; Khouri H.; Shetty J.; Berry K.;
RA Uterback T.; Tran K.; Wolf A.; Vamathevan J.; Ermolaeva M.; White O.;
RA Salzberg S.L.; Venter J.C.; Shapiro L.; Fraser C.M.;
RT *Complete genome sequence of Caulobacter crescentus.*;
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005709; AAK22345.1; -.
DR PIR; E87293; E87293.
DR TIGR; CC0358; -.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR008934; AcPase_VanPerase.
DR InterPro; IPR001011; Bac_AcPataaseA.
DR InterPro; IPR000326; PA_PTPase.
DR InterPro; IPR000437; Prok_lipoprot_S.
DR PRINTS; PR00483; BACPHPTASE.
DR PRODOM; PD009836; Bac_AcPataaseA; 1.
DR SMART; SM00014; acidPPc; 1.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 27634 MW; AAA962EF79AB9543 CRC64;

Query Match 21.5%; Score 274.5; DB 16; Length 258;
Best Local Similarity 34.6%; Pred. No. 9.fe-16;
Matches 80; Conservative 35; Mismatches 109; Indels 7; Gaps 7;

QY 13 LFSQALALVATGNDTTPKPLVYLNKSEAINSLALLPPPAVGSIAPFLNDQAMYEQRL 72
Db 6 LVTTAALMLTGCATLSGDAENRYLKG-VFDARDHLPPPAKGEALRDREIFRATRA 64

QY 73 LRNTERGKLAEDANLSSGGVANAFSGAFG-SPITEKDAPALEKLLNMIEDAGDLATRS 131
Db 65 LKDTPRWSLAQED-NVEE-KYLDGYACALGVTPSGFERN-PKLAVTLRLMSRDVRS-AVAG 120

QY 132 AKDHYMEIRPFAFYGVSTCNTTEQDKLSKNGSVPSGHTSIGWTALVLAIEINPORNEIL 191
Db 121 PKLYRPRPFYFSEEGPIC-IKRLGLALSDDYPSGHTATGWSVGLVLAIEVAPDRRAIL 179

QY 192 KRGVELQGSRVICGYHMQSDYDAARVVGSAVVATLHTNPAPFQOOLQAKAE 242
Db 180 ARAQAYGESRVVCGVHNSSVVEAGRMNAEKILSALKSSDAFKADLAARAE 230

Search completed: June 2, 2004, 10:46:58
Job time : 49 secs

GenCore version 5.1.6
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QM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 17:54:16 ; Search time 3428 Seconds
(without alignments)
15498.686 Million cell updates/sec

Title: US-09-807-990-1
Perfect score: 1225
Sequence: 1 ctcgacgcgaagcaatgt.....taagatcatgtgcggttaac 1225

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.ov.*
- 5: gb.pat.*
- 6: gb.ph.*
- 7: gb.pl.*
- 8: gb.pr.*
- 9: gb.ro.*
- 10: gb.sts.*
- 11: gb.sy.*
- 12: gb.un.*
- 13: gb.vi.*
- 14: em.ba.*
- 15: em.fun.*
- 16: em.hum.*
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- 18: em.mu.*
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- 30: em.htg.other.*
- 31: em.htg.mus.*
- 32: em.htg.pln.*
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- 35: em.htg.vrt.*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1225	100.0	1225	1	AB020481
2	1225	100.0	1225	6	BD014522
3	1225	100.0	1225	6	BD093734
4	750	61.2	750	6	AR140145
5	750	61.2	750	6	E16585
6	750	61.2	750	6	AR199634
7	750	61.2	750	6	BD017670
8	747	61.0	747	6	E12610
9	514.6	42.0	762	6	AR384033
10	512.2	41.8	1650	1	AB044338
11	507	41.4	747	6	AR140159
12	507	41.4	747	6	E16587
13	507	41.4	747	6	AR199648
14	507	41.4	747	6	BD017677
15	502.2	41.0	2198	1	AB044345
16	501.8	41.0	1322	1	KR250377
17	494.6	40.4	1650	6	BD014526
18	494.6	40.4	1650	6	BD093738
19	493.4	40.3	747	6	AR140160
20	493.4	40.3	747	6	E16588
21	493.4	40.3	747	6	AR199649
22	493.4	40.3	747	6	BD017678
23	423.6	34.6	1344	1	AB035805
24	423.6	34.6	1344	6	BD014523
25	423.6	34.6	1344	6	BD093735
26	422.4	34.5	1144	1	MMPHOC
27	422	34.4	750	6	AR140144
28	422	34.4	750	6	E16584
29	422	34.4	750	6	AR199633
30	422	34.4	750	6	BD017666
31	419	34.2	747	6	E12606
32	411.4	33.6	3626	12	ASPGREEN1
33	404.6	33.0	213494	1	SPFMR100
34	404.6	33.0	221618	1	AF386526
35	404.6	33.0	221851	1	AF348706
36	401.6	32.8	3633	12	ASPGREEN2
37	398	32.5	750	1	D82966
38	360.2	29.4	1036	1	PSPHONG
39	357.4	29.2	747	6	AR140158
40	357.4	29.2	747	6	E16586
41	357.4	29.2	747	6	AR199647
42	357.4	29.2	747	6	BD017676
43	304.6	24.9	735	6	AR140161
44	304.6	24.9	735	6	E16589
45	304.6	24.9	735	6	AR199650

ALIGNMENTS

RESULT 1
AB020481
LOCUS AB020481 1225 bp DNA linear BCF 20-JUN-2000
DEFINITION Escherichia blattae gene for acid phosphatase, complete cds.
ACCESSION AB020481
VERSION AB020481.1 GI:6003516
KEYWORDS acid phosphatase.
SOURCE Escherichia blattae
ORGANISM Escherichia blattae
REFERENCE 1 (sites)
AUTHORS Ishikawa,K., Mihara,Y., Gondoh,K., Suzuki,E. and Asano,Y.
TITLE X-ray structures of a novel acid phosphatase from Escherichia blattae and its complex with the transition-state analog mo: ybdate

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

EMBO J. 19 (11), 2412-2423 (2000)
20296667
10835340
2 (bases 1 to 1225)
Mihara, Y. and Asano, Y.
Direct Submission
Submitted (25-NOV-1998) Yasuhiro Mihara, Ajinomoto Co., Inc.,
Fermentation and Biotechnology Laboratory, Kawasaki-ku, Suzuki-cho,
1-1, Kawasaki-shi, Kanagawa 210-8681, Japan
(E-mail: bld.mihara@ajinomoto.co.jp, Tel: 81-44-244-7138,
Fax: 81-44-244-4757)

FEATURES

Location/Qualifiers

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/organism="Escherichia blattae"

/mol_type="genomic DNA"

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/db_xref="taxon:563"

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/translation="MKRVLAFTFAALFSSQALALVATGNDTTTKPDLVYLNSEAIN

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTGACGCGAAGCAATGTGTGTCGCGGTGAGCGGCACTCTACGAGATTAAAGATAAG 60

QY 61 TAATATCCATTATACAGTAACAGCAATGCTCTGAGTGTGATGTATACCTGAGCGG 120
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DB 121 CGCGGGGGTTCCTCCGCGCGCTTTTATGAGGCTGCGGTGAGGAGCGTTATCTGCTG 180

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DB 181 GCCCTGTTGTGCAACAACCGCTTTATGTTGTAATTTTGTGAGTATATCAGGTTTTT 240

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DB 241 AAGCACCTGTGGGCTCATACTGCAACCTGTTGATATTAAGCAACACTCTTCACTCAC 300

QY 301 GGAATTAACACGACAGTAAGGTATACGATGAATAAAGAGTTCTGGCAGTTGTTTT 360
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DB 421 AAACCGGATCTCTACTACTCAAGAACAGTGAAGCATTAACAGCGCTGGCGTGTGGCG 480

QY 481 CCACACGCGGGTGGGCTCCATGCGTTTCTCAAGCATCAGGCCATGTATGAACAGGGG 540
DB 481 CCACACGCGGGTGGGCTCCATGCGTTTCTCAAGCATCAGGCCATGTATGAACAGGGG 540

QY 541 CGCTCTGTCGCAACACCGAAGCGGTAACTGCGCGCGCAAGATGCAAACTCAGCAGT 600
DB 541 CGCTCTGTCGCAACACCGAAGCGGTAACTGCGCGCGCAAGATGCAAACTCAGCAGT 600

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DB 601 GCGGGGTGCGCAATGCTTTCTCGGCGCGTGTGGTAGCCGATCACCAGAAAGAGCGCC 660

QY 661 CCGCGCTGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 720
DB 661 CCGCGCTGCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720

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QY 781 AATACCAACGAGCAGGACAACTGTCGCAAAATGGCTCTTATCCGTCGGGCGATACCTCT 840
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QY 841 ATCGCTGCGCTACTGCGCTGCTGCGTGTGCTGCGCAGAGATCAACCTCAGCGCAGAGATC 900
DB 841 ATCGCTGCGCTACTGCGCTGCTGCGTGTGCTGCGCAGAGATCAACCTCAGCGCAGAGATC 900

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QY 961 GATGTGATGCGCGCGGCTGATGGGATCTCCGCTGTGGCGACCTGCTCATACCAACCGG 1020
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QY 1021 GCGTTCAGCAGCAGTTCGCAAGGCGAAGCGCAATTCGCGCCAGCATCAGAAGATAA 1080
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QY 1201 GCTATAGATCATGTGCGGTTAAC 1225
DB 1201 GCTATAGATCATGTGCGGTTAAC 1225

RESULT 2

BD014522 1225 bp DNA linear PAT 27-AUG-2002
LOCUS Variant nucleoside 5'-phosphate producing enzyme.

DEFINITION BD014522

ACCESSION BD014522

VERSION BD014522.1 GI:22555305

KEYWORDS JP 2001136984-A/1.

SOURCE Escherichia blattae

ORGANISM Escherichia blattae

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Escherichia.

1 (bases 1 to 1225)

Isikawa, K., Suzuki, E., Gondo, K., Shima, N., Mihara, Y., Kawasaki, H.,

Kurahashi, O., Koda, T., Shimaoka, M., Kozutsumi, R. and Asano, Y.

Variant nucleoside 5'-phosphate producing enzyme

Patent: JP 2001136984-A 1 22-MAY-2001;

AJINOMOTO CO INC

OS Escherichia blattae

PN JP 2001136984-A/1

PD 22-MAY-2001

PF 31-AUG-2000 JP 2000262120

PI KOKI ISHIKAWA, EIICHIRO SUZUKI, KEIKO GONDO, NOBUHISA SHIMBA, PI

YASUHIRO MIHARA,

[illegible]

QY	811	ATGTCCTTATCCGTCGGGATACCTCTATCGGCTGGGCTACGCTGGTGGTGGCA	870
DB	481	ATGTCCTTATCCGTCGGGATACCTCTATCGGCTGGGCTACGCTGGTGGTGGCA	540
QY	871	GAGATCAACCTCCAGCCGAGACGAGATCCCTGAACGCGGTATGAGCTGGGCCAGAGC	930
DB	541	GAGATCAACCTCCAGCCGAGACGAGATCCCTGAACGCGGTATGAGCTGGGCCAGAGC	600
QY	931	CGGTCATTTGGGCTACCACTGCGAGAGTGTGGATCCCGCGGGTGGTGGATCT	990
DB	601	CGGTCATTTGGGCTACCACTGCGAGAGTGTGGATCCCGCGGGTGGTGGATCT	650
QY	991	GCCGTTGTGGCGACCTTGATACCAACCCGCGGCTCCAGCAGAGTTGCGAAGCGAAG	1050
DB	651	GCCGTTGTGGCGACCTTGATACCAACCCGCGGCTCCAGCAGAGTTGCGAAGCGAAG	720
QY	1051	GCCGAAATTCGCCAGCATCAGAAATAA	1080
DB	721	GCCGAAATTCGCCAGCATCAGAAATAA	750
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DEFINITION	Escherichia blattae gene for acidic phosphatase.		
ACCESSION	E16585		
VERSION	E16585.1	GI:5711268	
KEYWORDS	JP 1998201481-A/2.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 750)		
AUTHORS	Mihara Y., Udagawa T., Yamada H. and Asano Y.		
TITLE	PRODUCTION OF NUCLEOSIDE 5'-PHOSPHATE		
JOURNAL	Patent: JP 199820148-A 2 04-AUG-1998;		
COMMENT	AJINOMOTO CO INC		
	OS Escherichia blattae		
	PN JP 1998201481-A/2		
	PD 04-AUG-1998		
	PF 18-JUN-1997 JP 1997161674		
	PI 21-NOV-1996 JP 96P 311103		
	PI MIHARA YASUHIRO, UDAKAWA TAKASHI, YAMADA HIDEAKI, PI ASANO		
	YASUHIRO		
	PC C12N15/09, C12N1/21, C12N9/16, C12P19/36, (C12N15/09, C12R1:01), PC		
	(C12N15/09, C12R1:22), (C12N15/09, C12R1:425), PC		
	PC (C12N1/21, C12R1:19), (C12N15/09, C12R1:19), (C12P19/36, C12R1:19);		
	CC (C12N9/16, C12R1:01), (C12N9/16, C12R1:19), (C12P19/36, C12R1:19);		
	CC topology: Double;		
	CC topology: Linear;		
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	FT	/strain='JCM 1650'	
	FT CDS	1..750	/product='acidic phosphatase' FT sig_peptide
	FT	1..54.	Location/Qualifiers
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			/mol_type='genomic DNA'
			/db_xref='taxon:32644'
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QY	391	CTGTCGCTACCGGAAACGACACTACCAAGAACCGGATCTCTACTACCTCAAGACAGT	450
DB	61	CTGTCGCTACCGGAAACGACACTACCAAGAACCGGATCTCTACTACCTCAAGACAGT	120
QY	451	GAAGCAATTAAACAGCCTGGCGTGTTCGCGCACCAACCGCGGTGGGCTCCATTCGCTTT	510
DB	121	GAAGCAATTAAACAGCCTGGCGTGTTCGCGCACCAACCGCGGTGGGCTCCATTCGCTTT	180
QY	511	CTCAACGATCAGGCCATGTATGAACAGGGGCGCTGTGCGCAACACCGAAGCGGTTAAG	570
DB	181	CTCAACGATCAGGCCATGTATGAACAGGGGCGCTGTGCGCAACACCGAAGCGGTTAAG	240
QY	571	CTGCGCGGAAAGATGCAAACTGACGACAGTGGCGGTGGCGAATGCTTTCTCCGCGCGC	630
DB	241	CTGCGCGGAAAGATGCAAACTGACGACAGTGGCGGTGGCGAATGCTTTCTCCGCGCGC	300
QY	631	TTTGTTAGCCCGATCACCGAAAAAGAGCCCGCGCTGCATAAATTAATCTGACCAATATG	690
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DB	361	ATTGAGGACGCGGGGATCTGCGCAACCGCGGCGGAAAGATCACTATATGCGCATTCGT	420
QY	751	CGTTGCGGTTTATGGGCTCTACCTGTATACCCAGCAGCAGACAAACTGTCCTAAA	810
DB	421	CGTTGCGGTTTATGGGCTCTACCTGTATACCCAGCAGCAGACAAACTGTCCTAAA	480
QY	811	ATGTCCTTATCCGTCGGGATACCTCTATCGGCTGGGCTACGCTGGTGGTGGCA	870
DB	481	ATGTCCTTATCCGTCGGGATACCTCTATCGGCTGGGCTACGCTGGTGGTGGCA	540
QY	871	GAGATCAACCTCCAGCCGAGACGAGATCCCTGAACGCGGTATGAGCTGGGCCAGAGC	930
DB	541	GAGATCAACCTCCAGCCGAGACGAGATCCCTGAACGCGGTATGAGCTGGGCCAGAGC	600
QY	931	CGGTCATTTGGGCTACCACTGCGAGAGTGTGGATCCCGCGGGTGGTGGATCT	990
DB	601	CGGTCATTTGGGCTACCACTGCGAGAGTGTGGATCCCGCGGGTGGTGGATCT	660
QY	991	GCCGTTGTGGCGACCTTGATACCAACCCGCGGCTCCAGCAGAGTTGCGAAGCGAAG	1050
DB	661	GCCGTTGTGGCGACCTTGATACCAACCCGCGGCTCCAGCAGAGTTGCGAAGCGAAG	720
QY	1051	GCCGAAATTCGCCAGCATCAGAAATAA	1080
DB	721	GCCGAAATTCGCCAGCATCAGAAATAA	750
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DEFINITION	Sequence 6 from patent US 6355472.		
ACCESSION	AR199634		
VERSION	AR199634.1	GI:20249708	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 750)		
AUTHORS	Mihara Y., Udagawa T., Yamada H. and Asano Y.		
TITLE	Method for producing nucleoside-5'-phosphate ester		
JOURNAL	Patent: US 6355472-A 6 12-MAR-2002;		
FEATURES	Location/Qualifiers		
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Best Local Similarity	100.0%;	Pred. No. 6.9e-198;	Indels 0;
Matches 750;	Conservative 0;	Mismatches 0;	Gaps 0;
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[illegible]

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DEFINITION    DNA encoding wild type acid phosphatase from Escherichia blattae.
ACCESSION     E12610
VERSION       E12610.1  GI:3251442
KEYWORDS      JP 1997037785-A/5.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 747)
AUTHORS      Mihara,Y., Udagawa,T., Yamada,H. and Asano,Y.
TITLE        PRODUCTION OF NUCLEOSIDE-5'-PHOSPHATE
JOURNAL      PATENT: JP 1997037785-A 5 10-FEB-1997;
COMMENT      AJINOMOTO CO INC
OS            Escherichia blattae
EN            JP 1997037785-A/5
ED            10-FEB-1997
PF            26-MAR-1996  JP 1996094680
PR            25-MAY-1995  JP 95P 149781
PI            MIHARA YASUHIRO, UDAGAWA TAKASHI, YAMADA HIDEAKI, PI ASANO
YASUHIRO
PC            C12N15/09,C12N9/16,C12P19/30,(C12N9/16,C12R1:19),(C12N9/16, PC
C12R1:01);
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CC            topology: linear;
CC            hypothetical: No;
CC            anti-sense: No;
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FT            Location/Qualifiers
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FEATURES
source
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Query Match          61.0%; Score 747; DB 6; Length 747;
Best Local Similarity 100.0%; Pred.No. 4.7e-197;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGAAAAACGTTCTGGCAGTTGTTTTCGGCATTGTTCTCTTCAGGCCCTGGCG 60
QY 391 CTGTTGCTACGGCAACGACACTACCAACGGAACGGATCTCTACTCTAAGAACAGT 450
DB 61 CTGTTGCTACGGCAACGACACTACCAACGGAACGGATCTCTACTCTAAGAACAGT 120
QY 451 GAAGCCATTACAGCTGGCGTGTTCGGCCACCAACGGCGGTGCTCCATTTCGGTT 510
DB 121 GAAGCCATTACAGCTGGCGTGTTCGGCCACCAACGGCGGTGCTCCATTTCGGTT 180
QY 511 CTCACGATCAGCCCATGTATGAACAGGGGGCGCTTGTCTGCGCAACACCGAGCGGTAG 570

181 CTCAACGATCAGGCCATGTATGAACAGGGGGCGCTTGTCTGCGCAACACCGAGCGGTAG 240
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931 CGGGTGATTTGCGGCTACCACTGGCAGAGTATGTGGATGCGCGCGGGTATGGGATCT 990
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991 GCCGTTGGCGACCCCTGCATACCAACCCGCGTTCCAGCAGAGCTTCAGAAAGCGAAG 1050
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1051 GCCGATTCGCCGAGCATCAGAAAGAA 1077
721 GCCGATTCGCCGAGCATCAGAAAGAA 747

RESULT 9
AR384033
LOCUS          AR384033          762 bp    DNA          linear          PAT 18-DEC-2003
DEFINITION    Sequence 762 from patent US 6610836.
ACCESSION     AR384033
VERSION       AR384033.1  GI:40093767
KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 762)
AUTHORS      Breton,G.L. and Osborne,M.
TITLE        Nucleic acid amino acid sequences relating to Klebsiella pneumoniae
              for diagnostics and therapeutics
JOURNAL       Patent: US 6610836-A 762 26-AUG-2003;
FEATURES      Location/Qualifiers
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              /mol_type='genomic DNA'

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Best Local Similarity 79.8%; Pred.No. 3.5e-132;
Matches 607; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

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377 CTCAGGCCCTGGCGTGGTTCGCTACCGCAACGACACTACCAAGAAACCGGATCTTACT 436
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 242 CCGAGCGGGGAAGTGGCGGCGAGAGATGCCAACTCAGCGCGGGCGCTGGCGAAGC 301
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 857 CGTGTGTGTCGAGAGATCAACCTCAGCGCGCAGAACGAGATCTGAAACCGGTTATG 916
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 917 AGCTGGCGCAGACCGCGGTGATTTGGCGGTACACCTGGGAGAGATGTTGGATCGCGCG 976
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 AB044338
 AB044338.1 GI:11610578
 Enterobacter aerogenes
 Enterobacter aerogenes
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Enterobacter.
 1 (sites)
 Miura, Y., Utagawa, T., Yatsui, H. and Asano, Y.
 Acid phosphatase/phosphotransferase from enteric bacteria
 Unpublished
 2 (bases 1 to 1650)
 Miura, Y. and Asano, Y.
 Direct Submission
 Submitted (06-JUN-2000) Yasuhiro Miura, Ajinomoto Co., Inc.,
 Fermentation & Biotechnology laboratories; Kawasaki-Ku,
 Kawasaki-shi, Kanagawa 210-8681, Japan
 (E-mail: yasuhiro.miura@ajinomoto.com, Tel: 81-44-244-7138,
 Fax: 81-44-244-4757)
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Query Match 41.8%; Score 512.2; DB 1; Length 1650;
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FEATURES
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RESULT 11
LOCUS AR140159
DEFINITION Sequence 23 from patent US 6207435.
ACCESSION AR140159
VERSION AR140159.1 GI:14482655
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 747)
AUTHORS Mihara, Y., Udagawa, T., Yamada, H. and Asano, Y.
TITLE Method for producing nucleoside-5'-phosphate ester
JOURNAL Patent: US 6207435-A 23 27-MAR-2001;
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    Best Local Similarity 79.9%; Pred. No. 4.7e-130;
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LOCUS E16587
DEFINITION Enterobacter aerogenes gene for acidic phosphatase.
ACCESSION E16587
VERSION E16587.1 GI:5711270
KEYWORDS JP 1998201481-A/4.
SOURCE Enterobacter aerogenes
ORGANISM Enterobacter aerogenes
REFERENCE 1 (bases 1 to 747)
AUTHORS Mihara, Y., Udagawa, T., Yamada, H. and Asano, Y.
TITLE PRODUCTION OF NUCLEOSIDE 5'-PHOSPHATE
JOURNAL Patent: JP 1998201481-A 4 04-AUG-1998;
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    Query Match 41.4%; Score 507; DB 6; Length 747;
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    Matches 597; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
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Unknown.
Unknown.
Unclassified.
1 (bases 1 to 747)
Unclassified.
Mihara, Y., Utagawa, T., Yamada, H. and Asano, Y.
Method for producing nucleoside-5'-phosphate ester
Patent: US 635472-A 23 12-MAR-2002;
Location/Qualifiers
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DEFINITION		Mutant acidic phosphatase.				
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VERSION		BD017677.1	GI:22558853			
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AUTHORS		Mibar, Y.; Udagawa, T., Yamada, H. and Asano, Y.				
TITLE		Mutant acidic phosphatase				
JOURNAL		Patent: JP 2001245676-A 12 11-SEP-2001;				
		ATKINSON CO INC				

[illegible]

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Job time : 3431 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 3373863 seqs, 2124099041 residues

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28	39.6	3.2	1830	7	ACA37565	ACA37565 Prokaryot
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ALIGNMENTS

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DT 23-JUL-2001 (first entry)
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Variant nucleoside-5'-phosphate producing enzyme; mutagenesis;
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X-ray structural analysis; three-dimensional structure; ds.

Escherichia blatae.

WO200118184-A1.

15-MAR-2001.

01-SEP-2000; 2000WO-JP005973.

03-SEP-1999; 95JP-00249545.

(AJIN) AJINOMOTO CO INC.

Ishikawa K, Suzuki E, Gondoh K, Shimba N, Mihara Y, Kawasaki H;
Kurashiki O, Kouda T, Shimaoka M, Kozutsumi R, Asano Y;

WPI; 2001-380914/40.

P-PSDB; AAB75064.

Variant enzyme having elevated nucleoside 5'-prime phosphate producing
activity and having a specific three-dimensional structure for production
of nucleotides as pharmaceutical intermediates.

Disclosure; Page 105-106; 150pp; Japanese.

The present invention describes a variant nucleoside-5'-phosphate
producing enzyme which is a modification of a transphosphorylase or
phosphatase which contains a lysine, two arginine and two histidine
residues and in which the C-alpha distances between these residues are
enclosing a space which permits the binding of a nucleoside with these
residues. Also described are: (1) a gene encoding the variant enzyme; (2)
expression vectors containing the DNA; (3) host cells transformed by the
vectors; (4) preparation of the variant enzyme by culture of the

CC phosphatase (AP), which can be used to produce a nucleoside 5'-phosphate
CC ester from the corresponding nucleoside when a phosphate donor, e.g. poly
CC -, phenyl- or carbamyl-phosphoric acid, is reacted in its presence at pH
CC 3.0 to 5.5. The PA can be used for the economic and efficient production
CC of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals
CC and intermediates for pharmaceuticals
XX
SQ Sequence 750 BP; 170 A; 212 C; 217 G; 151 T; 0 U; 0 Other;
Query Match 61.2%; Score 750; DB 2; Length 750;
Best Local Similarity 100.0%; Pred. No. 3.4e-225;
Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 331 ATGAAAAAGCTGCTGGCAGTTTGTGTCGCGCATTTCTTCTCAGGCGCTGGCG 390
DB 1 ATGAAAAAGCTGCTGGCAGTTTGTGTCGCGCATTTCTTCTCAGGCGCTGGCG 60
QY 391 CTGGTCGCTACCGGCAACGACACTACCAAGAAACCGGATCTCTACTACCTCAAGAACGT 450
DB 61 CTGGTCGCTACCGGCAACGACACTACCAAGAAACCGGATCTCTACTACCTCAAGAACGT 120
QY 451 GAAGCCATTAAACAGCTGGCGCTGTTGCGCGCACACGCGGCTGGCGCTGGCGTTT 510
DB 121 GAAGCCATTAAACAGCTGGCGCTGTTGCGCGCACACGCGGCTGGCGCTGGCGTTT 180
QY 511 CTCAACGATCAGGCGCATGTATGAACAGGCGCGCTGCTGGCGCAACCGGAGCGGTAAG 570
DB 181 CTCAACGATCAGGCGCATGTATGAACAGGCGCGCTGCTGGCGCAACCGGAGCGGTAAG 240
QY 571 CTGGCGCGGAAGATGCAAACTGAGCAGTGGCGGCTGGCGGTAAGTCTTCTCCGCGCG 630
DB 241 CTGGCGCGGAAGATGCAAACTGAGCAGTGGCGGCTGGCGGTAAGTCTTCTCCGCGCG 300
QY 631 TTGCGTACCGGATCACCAGAAAGAGCGCGGCTGGCGGTAAGTCTTCTCCGCGCG 690
DB 301 TTGCGTACCGGATCACCAGAAAGAGCGCGGCTGGCGGTAAGTCTTCTCCGCGCG 360
QY 691 ATTGAGGACGCGCGGATCTGGCGACCGGCGCGGCGGAAAGATCACTATATCGCATTCGT 750
DB 361 ATTGAGGACGCGCGGATCTGGCGACCGGCGCGGCGGAAAGATCACTATATCGCATTCGT 420
QY 751 CCGTTCGGTTTATGCGGCTCTTACCTGTATATACCGGAGCGGAGCAAACTGTCCAAA 810
DB 421 CCGTTCGGTTTATGCGGCTCTTACCTGTATATACCGGAGCGGAGCAAACTGTCCAAA 480
QY 811 AATGGCTTTATCGTGGCGCATACCTCTATCGGCTGGCTACTGCGCTGGTCTGGCA 870
DB 481 AATGGCTTTATCGTGGCGCATACCTCTATCGGCTGGCTACTGCGCTGGTCTGGCA 540
QY 871 GAGATCAACCTTCAGCGCGCAGAACGAGATCCTGAAACCGGTTATGACTGGGCGAGCG 930
DB 541 GAGATCAACCTTCAGCGCGCAGAACGAGATCCTGAAACCGGTTATGACTGGGCGAGCG 600
QY 931 CGGCGATTTCGGGTACCACTGGCAGAGTGAATGAGTGGCGCGGCTAGTGGGATCT 990
DB 601 CGGCGATTTCGGGTACCACTGGCAGAGTGAATGAGTGGCGCGGCTAGTGGGATCT 660
QY 991 GCGGTTGTGGGACCTCGATACCAACCGCGGTTCCAGAGCAGTTCAGAAACCGAAG 1050
DB 661 GCGGTTGTGGGACCTCGATACCAACCGCGGTTCCAGAGCAGTTCAGAAACCGAAG 720
QY 1051 GCCGAATTGCGCGGATCAGAAAGATAAA 1080
DB 721 GCCGAATTGCGCGGATCAGAAAGATAAA 750
RESULT 3
AAV43046
ID AAV43046 standard; DNA; 750 BP.
XX AC
XX AAV43046;
XX
DT 21-OCT-1998 (first entry)

XX DNA encoding an acid phosphatase enzyme.
DE Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
KW intermediate; ds.
XX
OS Escherichia blattae.
XX
FH Key Location/Qualifiers
CDS 1..750
FT /*tag= a
FT sig_peptide 1..54
FT /*tag= b
FT mat_peptide 55..747
FT /*tag= c
XX
EP857788-A2.
XX
PD 12-AUG-1998.
XX
XX 20-NOV-1997; 97EP-00309365.
XX
PR 21-NOV-1996; 96JP-00311103.
PR 18-JUN-1997; 97JP-00161674.
XX
PA (AJIN) AJINOMOTO CO INC.
XX
XX Mihara Y, Utagawa T, Yamada H, Asano Y;
XX
XX WPI: 1998-416010/36.
XX P-PSDE; RAW71029.
XX
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX with phosphate donor in presence of acid phosphatase - used as seasonings
XX or pharmaceutical intermediates.
XX
XX Example 12; Page 34-35; 83pp; English.
XX
XX The present sequence encodes an acid phosphatase enzyme. The
XX specification describes a method for the preparation of nucleoside 5'-
XX phosphate esters. The method comprises reacting a nucleoside with a
XX phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
XX has been altered to increase its affinity for the nucleoside and/or to
XX increase its thermal stability, or in the presence of a microorganism
XX that has been transformed with recombinant DNA containing a gene coding
XX for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
XX seasonings or pharmaceuticals or as intermediates for them
XX
SQ Sequence 750 BP; 170 A; 212 C; 217 G; 151 T; 0 U; 0 Other;
Query Match 61.2%; Score 750; DB 2; Length 750;
Best Local Similarity 100.0%; Pred. No. 3.4e-225;
Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 331 ATGAAAAAGCTGCTGGCAGTTTGTGTCGCGCATTTCTTCTCAGGCGCTGGCG 390
DB 1 ATGAAAAAGCTGCTGGCAGTTTGTGTCGCGCATTTCTTCTCAGGCGCTGGCG 60
QY 391 CTGGTCGCTACCGGCAACGACACTACCAAGAAACCGGATCTCTACTACCTCAAGAACGT 450
DB 61 CTGGTCGCTACCGGCAACGACACTACCAAGAAACCGGATCTCTACTACCTCAAGAACGT 120
QY 451 GAAGCCATTAAACAGCTGGCGCTGTTGCGCGCACACGCGGCTGGCGCTGGCGTTT 510
DB 121 GAAGCCATTAAACAGCTGGCGCTGTTGCGCGCACACGCGGCTGGCGCTGGCGTTT 180
QY 511 CTCAACGATCAGGCGCATGTATGAACAGGCGCGCTGCTGGCGCAACCGGAGCGGTAAG 570
DB 181 CTCAACGATCAGGCGCATGTATGAACAGGCGCGCTGCTGGCGCAACCGGAGCGGTAAG 240
QY 571 CTGGCGCGGAAGATGCAAACTGAGCAGTGGCGGCTGGCGGTAAGTCTTCTCCGCGCG 630
DB 241 CTGGCGCGGAAGATGCAAACTGAGCAGTGGCGGCTGGCGGTAAGTCTTCTCCGCGCG 300

QY 631 TTGTGACCGGATCACGAAAGAGCGCCCGGCTGCATATATCTACGACCAATATG 690
 DB 301 TTGTGACCGGATCACGAAAGAGCGCCCGGCTGCATATATCTACGACCAATATG 360
 QY 651 ATTGAGGAGCGCGGGATCTGGCGACCGCGAGCGGAAAGATCACTATATGCGCAATCGT 750
 DB 361 ATTGAGGAGCGCGGGATCTGGCGACCGCGAGCGGAAAGATCACTATATGCGCAATCGT 420
 QY 751 CCGTTCGGCTTTTATGCGGTCTCTACCTGTATATACACCGAGCGGACAACTCTCCAAA 810
 DB 421 CCGTTCGGCTTTTATGCGGTCTCTACCTGTATATACACCGAGCGGACAACTCTCCAAA 480
 QY 811 ATGCTCTTATCCGTCGGGCATACCTCTATCGGCTGGCTACTCGCTGGTGTGGCA 870
 DB 481 ATGCTCTTATCCGTCGGGCATACCTCTATCGGCTGGCTACTCGCTGGTGTGGCA 540
 QY 871 GAGATCAACCTCTAGCGCCAGAACGAGATCTTGAACCGCGTTATGAGCTGGGCCAGAGC 930
 DB 541 GAGATCAACCTCTAGCGCCAGAACGAGATCTTGAACCGCGTTATGAGCTGGGCCAGAGC 600
 QY 931 CCGGTGATTTGGCTTACACTGGGAGATGATGTGATGCGCGCGGCTAGTGGATCT 990
 DB 601 CCGGTGATTTGGGCTTACACTGGGAGATGATGTGATGCGCGCGGCTAGTGGATCT 660
 QY 991 GCGGTGCGGACCTCGATACCAACCGCGCTTCCAGCAGCAGTTGCAGAAAGCGAAG 1050
 DB 661 GCGGTGCGGACCTCGATACCAACCGCGCTTCCAGCAGCAGTTGCAGAAAGCGAAG 720
 QY 1051 GCGGAATTCGCCAGCATCAGAAATAA 1080
 DB 721 GCGGAATTCGCCAGCATCAGAAATAA 750

RESULT 4

AA745007

ID AAT45007 standard; DNA; 747 BP.

XX AC AAT45007;

XX DT 13-AUG-1997 (first entry)

XX DE Enterobacter aerogenes IFC 12010 acid phosphatase DNA.

XX KW IFC 12010; acid phosphatase; production; nucleoside; 5'-phosphate; ester;

XX OS condiment; pharmaceutical; intermediate; ds.

XX OS Enterobacter aerogenes.

XX FH Key Location/Qualifiers

XX FT CDS 1..747

XX FT FT /**tag= a

XX FT FT /product= "acid_phosphatase"

XX FT FT

XX PN WC9637603-A1.

XX PD 28-NOV-1996.

XX PF 24-MAY-1996; 96WO-JP001402.

XX PR 25-MAY-1995; 95JP-00149781.

XX PR 26-MAR-1996; 96JP-00094680.

XX XX

XX PA (AJIN) AJINOMOTO CO INC.

XX PI Minhara Y, Utogawa T, Yamada H, Asano Y;

XX DR WPI; 1997-021215/02.

XX DR P-PSDB; AAW06458.

XX XX

XX PT Efficient production of nucleoside 5'-phosphate - by reaction of a

XX PT nucleoside with a phosphoric acid donor in the presence of an acid

XX PT phosphatase.

XX

Example 24; Page 67-68; 95pp; Japanese.

XX The present sequence encodes the Enterobacter aerogenes IFC 12010 acid
 CC phosphatase (AP), which can be used to produce a nucleoside 5'-phosphate
 CC ester from the corresponding nucleoside when a phosphate donor, e.g. poly
 CC -, phenyl- or carbamyl-phosphoric acid, is reacted in its presence at pH
 CC 3.0 to 5.5. The PA can be used for the economic and efficient production
 CC of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals
 CC and intermediates for pharmaceuticals

SQ Sequence 747 BP; 181 A; 210 C; 205 G; 151 T; 0 U; 0 Other;

Query Match 41.4%; Score 507; DB 2; Length 747;

Best Local Similarity 79.9%; Pred. No. 1.2e-148;

Matches 597; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 331 ATGAAAACGTTCTGCGAGTTGTTTGGCGCATTTGTTCTCTCAGGCCCTGGCG 390

DB 1 ATGAAAACGCGTTCTCGCCCTCTGCTGCGCGCTGTTTCCGTTACGTTTGGCG 60

QY 391 CTGGTCGTACCGGCAACGACACTACCGGAAACCGGATCTCTACTACCTCAGAACAGT 450

DB 61 CTGGTCCTCGCGCAATGATGCAACCAACCAACCGGATCTCTATTATCTGAAAAATGCA 120

QY 451 GAAGCATTAACAGCTGCGGCTGTTGCGCGCAACCGCGGCTGCGCTCCATGCGTTT 510

DB 121 CAGGCCATCGATAGTCTGCGGCTGTTGCGCGCGCGCGCGGAGTTGGCAGCATCGCATTT 180

QY 511 CTCAAGCATCAGGCCATGATGAACAGGGGCGCTGCTGGCGCAACCGCAACCGGTAAG 570

DB 181 TTAACGATCAGCGGATGATGAAGAGAGCGGCTGTTGGCAATACCGAACGTTGGCAAG 240

QY 571 CTGGCGCGGAGATGCAACCTGAGCAGTGGGGGTTGGCGGATGTTCTTCGCGGCGG 630

DB 241 CTGGCGGCTGAAGATGCTAAGCTGAGCGCGCGGCGGCTGCGGATGCTTCCAGCGCT 300

QY 631 TTTGGTAGCCGATACCGAAAGAGCGCCCGCGGCTGCAATAATTAATGACCAATATG 690

DB 301 TTTGGTTGCGCCATCACCGAAAGAGCGCGCGGAGTTACATAAGCTGCTGACAAATAG 360

QY 691 ATTGAGGAGCGCGGATCTGGGAGCGCGGAGGAGATCACTATATCGCATTCGT 750

DB 361 ATTGAGGATCGCGGATCTGGCCCGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGG 420

QY 751 CCGTTCCGCTTTATGGGGTCTCTACCTGTAATACCGAGCAGGACAACTGTCCTAAA 810

DB 421 CCGTTTGGTTCTACGGGTTTCAACCTGTAACACTACCGAGCAGGACAGCTGTGAAA 480

QY 811 AATGGCTTTATCCGTCGGGCTACCTCTATCGGCTGGGCTACTCGCTGTGCTGCGCA 870

DB 481 AACGGATCTTACCCCTTCGGGCTACCTCTATCGGTTGGGCAACCGCGCTGTGATCTGGCG 540

QY 871 GAGATCAACCTCAGCGCCAGAACGAGATCTGAAACCGCGGTTATGAGCTGGCGCAGAGC 930

DB 541 GAGATCAATCCGAGCGGCAAAAGAAATTCCTCAACCGCGCTATGATTTGGCGGAAAGC 600

QY 931 CCGGTGATTTGCGGCTACCACTGCGCAGAGTATGTTGATGCGCGCGGCTAGTGGATCT 990

DB 601 CCGGTATCTCGGCTATCATTTGGCAGAGCGATGTCGATGCGGCGCGGATAGTCGGCTCG 660

QY 991 GCCGTTGTGGGACCTGCGATACCAACCGCGGTTCCAGCAGCAGGATTCAGAAAGCGAAG 1050

DB 661 GCCGTTGTGGGACCTGCGATACCAACCGCGGCTTCCAGCAGCAGGATTCAGAAAGCGAAG 720

QY 1051 GCCGAATTCGCCAGCATCAGAAATAA 1077

DB 721 GATGAATTCGCCAAAGACGAGAGTAA 747

RESULT 5

AAV43060

ID AAV43060 standard; DNA; 747 BP.

XX AAV43060;
 AC 21-OCT-1998 (first entry)
 XX DNA encoding an acid phosphatase enzyme.
 DE
 XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 XX intermediate; ds.
 KW
 XX Enterobacter aerogenes.
 OS
 XX
 PE Key Location/Qualifiers
 FT 1. 747
 FT /*tag= a
 XX
 PN EF857788-A2.
 XX
 XX 12-AUG-1998.
 XX
 XX 20-NOV-1997; 97EP-00309365.
 XX
 XX 21-NOV-1996; 96JP-00311103.
 PR 18-JUN-1997; 97JP-00161674.
 XX
 XX (AJIN) AJINOMOTO CO INC.
 PA
 XX Mihara Y, Utagawa T, Yamada H, Asano Y;
 PI
 XX WPI; 1998-416010/36.
 XX P-PSDB; AAW71031.
 DR
 XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 PT with phosphate donor in presence of acid phosphatase - used as seasonings
 PT or pharmaceutical intermediates.
 PT
 XX
 XX Example 24; Page 43; 83pp; English.
 PS
 XX The present sequence encodes an acid phosphatase enzyme. The
 CC specification describes a method for the preparation of nucleoside 5'-
 CC phosphate esters. The method comprises reacting a nucleoside with a
 CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
 CC has been altered to increase its affinity for the nucleoside and/or to
 CC increase its thermal stability, or in the presence of a microorganism
 CC that has been transformed with recombinant DNA containing a gene coding
 CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
 CC seasonings or pharmaceuticals or as intermediates for them
 XX
 XX Sequence 747 BP; 181 A; 210 C; 205 G; 151 T; 0 U; 0 Other;
 SQ
 Query Match 41.4%; Score 507; DB 2; Length 747;
 Best Local Similarity 79.9%; Pred. No. 1.2e-148;
 Matches 597; Conservative 0; Mismatches 150; Indels 0; Gaps 0;
 QY 331 ATGAAAGACGTTCTGCGAGTTGTTTTCGCGATTGTTCTCTCTCAGGCCCTCGCG 390
 DB 1 ATGAAAGACGTTCTGCGAGTTGTTTTCGCGATTGTTCTCTCTCAGGCCCTCGCG 60
 QY 391 CTGTCGCTACCGGACGACACTACACGAGAACCGGATCTCTACTACTCAAGAACAGT 450
 DB 61 CTGTCGCTCGCGGATGATGATGACACCAACCGGATCTCTATTATCTGAAAAATGCA 120
 QY 451 GAAGCCATTAACAGCTCGCGCTGTTGCGCCACCCACCGCGGCTCGCATTCGCTTT 510
 DB 121 CAGCCATTCGATGTTCTGCGCTGTTGCGCGCGCGCGGAGTTGGAGCATTCGCAATT 180
 QY 511 CTCACGATCAGGCCATGATGAAACAGGCGCGCTGTCGCGCAACACCGAGCGGTAAG 570
 DB 181 TTAACGATCAGCGGATGATGAGAAAGGACGCGCTGTTGCGCAATACCGAACGTCGCAAG 240
 QY 571 CTGCGCGCGGAGATGCAAACTGAGCAGTGGCGGGTGGCGAATGCTTCTCCGCGCG 530
 DB 241 CTGCGCGCTGAAGATGCTAACTGAGCGCGCGCGCTGCGAATGCTTCTTCCAGCGCT 300

QY 631 TTTGGTAGCCGATCACCAGAAAGAGCCCGCGCTGCATAAATTACTGACCAATATG 690
 DB TTTGGTTCCGCATCACCAGAAAGAGCGCGCGAGTTACATAAGCTGCTGCAATATG 360
 QY 691 ATTGAGGACGCGGGGATCTGGGACCCCGCAGCGCGAAAGATCATATATCGCATTCGT 750
 DB ATTGAGGATGCGGCGATCTGGCCACCGCGAGCGGAAAGAAATATATCGCATTCGC 420
 QY 751 CCGTTCCGCTTTATGGGCTCTACCTGTAATACCCGAGCAGGACAACTGTCCAAA 810
 DB CCGTTCCGCTTCTACGGGCTTTCAACCTGTAACTACCGAGCAGGACAGCTGTGAAA 480
 QY 811 AATGCTCTTATCCGTCGGGCATACCTCTATCGGCTGGGCTACTGCGCTGGTGTGCA 870
 DB AACGATCTTACCTTTCGGCCATACCTCTATCGTTGGGCAACCGCGCTGGTACTGCG 540
 QY 871 GAGATCAACCTCAGCGCAGAACGAGATCTGAAAACGCGTTATGACTGGGCCAGAGC 930
 DB GAGATCAATCGCAGCGCAAAACGAAATTTCTAAACGCGCTATGAATTGGGCGAAAGC 600
 QY 931 CGGTTGATTTTCGGCTACCTGCGCAGATGATGTGGATCGCGCGGCTAGTGGGATCT 990
 DB CGGTTATCTCGGCTATCATTTGGCAGAGCGATGTGATGCGCGCGGATGCTGCTCG 660
 QY 991 GCCGTTGTGCGACCTCTGCATACCAACCCGCGCTTCCAGCAGCAGTTCCAGAAACGAG 1050
 DB GCGTGTGTGCGACCTCTGCATACCAACCCGCGCTTCCAGCAGCAGTTCCAGAAACGAG 720
 QY 1051 GCCGAATTCGCCAGCATCAGAGAAA 1077
 DB GATGAATTCGCCAAACGCGAGAGTAA 747

RESULT 6

AAH19705
 ID AAH19705 standard; DNA; 1450 BP.

XX AC AAH19705;

XX DT 23-JUL-2001 (first entry)

XX Enterobacter aerogenes nucleotide-5'-phosphate producing enzyme DNA.

XX Variant nucleoside-5'-phosphate producing enzyme; mutagenesis;

XX transphosphorylation; phosphatase; protein co-ordinate data;

XX X-ray structural analysis; three-dimensional structure; ds.

XX OS Enterobacter aerogenes.

XX WO200118184-A1.

XX PD 15-MAR-2001.

XX PF 01-SEP-2000; 2000WO-JP005973.

XX PR 03-SEP-1999; 99JP-00249545.

XX (AJIN) AJINOMOTO CO INC.

XX Ishikawa K, Suzuki E, Gondoh K, Shimba N, Mihara Y, Kawasaki H;

PI Kurahashi O, Kouda T, Shimaoka M, Kozutsumi R, Asano Y;

XX WPI; 2001-380914/40.

DR P-PSDB; AAB75068.

XX Variant enzyme having elevated nucleoside 5'-prime phosphate producing
 PT activity and having a specific three-dimensional structure for production
 PT of nucleotides as pharmaceutical intermediates.

XX Disclosure; Page 115-117; 150pp; Japanese.

XX The present invention describes a variant nucleoside-5'-phosphate

181 TTAACGATCAGCGATGATGAGAAGCGCGTCTCTCGCGCCACCGCCGCGCAAG 240
571 CTGGCGCGGAGATCAAACTTGAGCAGTGGCGGGTGGCAATGCTTTCTCGCGCG 630
241 TTGGCGCGGAGATGCAACCTGAGCGCGGTGGCGTGGCCAAACGCTTCTCGCGCA 300
631 TTGGTAGCGCGATCACCGAARAAGCGCCCGCGCTGCGATTAATACGACCAATATG 690
301 TCGCGTCCCGATCAGCAAAAGAGCGCCCGCGCTGCACAACTGCTCACCAATG 360
691 ATTGAGACCGCGGGATCTGGCACCGCGAGCGGAAAGATCACTATATGCGGATCGT 750
361 ATTGAGACCGCGGATCTGGCACCGCGAGCGGAAAGATGATATGCGGATTCGT 420
751 CCGTTCGCGTTTATGGGCTCTACCTGTAAATACACCGAGAGGACAACTGTCAAA 810
421 CCGTTTGCCTTCTACGCGGTGTCACCTGCAATACCAACGAGAGATGCTGCAAA 480
811 AATGGCTCTTATCGTCGCGGATACCTCTATCGCTGGGCTACTGCGTGGTCTGGCA 870
481 AAGCGCTCTTACCGCTTCCGGACACACCTCTATCGCTGCGGACCGCCCTGCTGCC 540
871 GAGATCAACCTCAGCGCCAGACGAGATCTGAAACCGGTTATGAGCTGGGCCAGAGC 930
541 GAAATCAACCGCAGCGCCAGATGAGATTCTCAAGCGCGGCTATGAGCTCGGTGAAAGT 600
931 CCGGTGATTTGGGCTACCACTGCGAGAGTATGAGTGGATGGCGCGGTTAGTGGATCT 990
601 CCGGTGATTTGGGCTACCACTGCGAGAGTATGAGTGGATGGCGCGGTTAGTGGATCT 660
991 GCGGTGTTGGGCGACCTGCTATACCAACCGCGGTTCAGAGAGAGTTCGCAAAAGCGAAG 1050
661 GCGGTGTTGGGCGACCTGCTATACCAACCGCGGTTCAGAGAGAGTTCGCAAAAGCGAAG 720
1051 GCCGAATTGGCCAGCATCAGAA 1073
721 GACGAGTTGGAAACAGCAGAA 743

RESULT 8
AAV43061
ID AAV43061 standard; DNA; 747 BP.
XX AAV43061;
AC AAV43061;
XX AAV43061;
XX AAV43061;
DT 27-AUG-2003 (revised)
DT 21-OCT-1998 (first entry)
XX DNA encoding an acid phosphatase enzyme.
XX Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
KW intermediate; ds.
XX Raoultella planticola.
XX Key Location/Qualifiers
FT CDS 1..747
FT /*tag= a
XX
XX EP857788-A2.
XX
XX 12-AUG-1998.
XX
XX 20-NOV-1997; 97EP-00309365.
XX
XX 21-NOV-1996; 96JP-00311103.
PR 18-JUN-1997; 97JP-00161674.
XX
XX (AJIN) AJINOMOTO CO INC.
XX
XX Miura Y, Utogawa T, Yamada H, Asano Y;
PI WPI; 1998-416010/36.
XX
XX

P-PSDB; AAW71032.
XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
PT with phosphate donor in presence of acid phosphatase - used as seasonings
PT or pharmaceutical intermediates.
XX
XX Example 24; Page 45-46; 83pp; English.
PS
XX The present sequence encodes an acid phosphatase enzyme. The
CC specification describes a method for the preparation of nucleoside 5'-
CC phosphate ester. The method comprises reacting a nucleoside with a
CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
CC has been altered to increase its affinity for the nucleoside and/or to
CC increase its thermal stability, or in the presence of a microorganism
CC that has been transformed with recombinant DNA containing a gene coding
CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
CC seasonings or pharmaceuticals or as intermediates for them. note: this
CC sequence appears to be claimed (Claim 6), but as the claim refers to
CC amino acid sequences, it is clear that the corresponding protein is
CC being claimed. (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 747 BP; 168 A; 230 C; 209 G; 140 T; 0 U; 0 Other;
SQ
Query Match 40.3%; Score 493.4; DB 2; Length 747;
Best Local Similarity 79.0%; Pred. No. 2.2e-144;
Matches 587; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
QY 331 ATGAAAAACCTGTTCTGGCAGTTTGTGTCGCAATTGTTCTTCTCAGGCCCTTGGCG 390
Db 1 ATGAAAAAGCGTGTACTGCGCTTGTGCTTGGCAGCTTCTTTCAGTAGCGCTTGGCG 60
QY 391 CTGTGCTGCTACCGCAACGACACTACCAAGAACCGGATCTCTACTCTCAAGACAGT 450
Db 61 CTGTGCTGCGCGCAATGATGCCACCAACGCGGATCTCTACTCTCAAAATGCC 120
QY 451 GAAGCCATTACAGCTGCGCTGTGGCGCCACCAACCGCGGCTGCTTCCATTTGGTTT 510
Db 121 CAGGCCATTGACAGCTGCGCTGTGGCACCGCGCGGAGTGGCGAGCATTTGGTTT 180
QY 511 CTCACGATCAGCGCATGTATGAACAGGGCGCGCTGCTGCGCAACACCGGTAAG 570
Db 181 TTAACGATCAGCGCATGTATGAAGAGCCCTGCTGCGCGCCACCGCGCGCAAG 240
QY 571 CTGGCGCGGAGATGCAAACTGAGCAGTGGCGGGTGGCAATGCTTTCTCGCGCG 630
Db 241 TTGGCGCGGAGATGCCAACCTGAGCGGGTGGCGTGGCCAAACGCTTCTCGCGCA 300
QY 631 TTTGTTAGCCCGATCACCGAANAAGACCGCGCGCTGCATAAATTTACTGACCAATATG 690
Db 301 TTGCGCTCCCGATCAGCGAANAAGACCGCGCGGCTGCACAACTGCTCACCAATG 360
QY 691 ATTGAGGACCGCGGATCTGCGACCGCGCGGATGATATATGCGCATTCGT 750
Db 361 ATTGAGACCGCGGCGATCTGCGACCGCGCGGAGAGAGATATATGCGTATTCGT 420
QY 751 CCGTTGCGCTTTTATGGGCTCTCTACTCTGCGCTGGGCTACTGCGTGGTCTGGCA 810
Db 421 CCGTTGCGCTTCTACGCGGTGTCACCTGCAATACCAACCGAAGAGATGCTGCAAA 480
QY 811 AATGGCTCTTATCGCTGCGGCGATACCTCTATCGGCTGGGCTACTGCGTGGTCTGGCA 870
Db 481 AACGGCTCTTACCTTCCGACACACCTCTATCGGCTGGGCGACCGCCCTGCTGGCC 540
QY 871 GAGATCAACCTCAGCGCCAGAACGAGATCTTGAACCGCGTTATGAGCTGGGCCAGAGC 930
Db 541 GAAATCAACCGCAGCGCCAGATGAGATTCTCAAGCGCGGCTATGAGCTCGGTGAAAGT 600
QY 931 CCGGTGATTTGGGCTACCACTGCGAGAGTATGATGATGCGCGCGGTAGTGGGATCT 990
Db 601 CCGGTGATCTGCGGTTACCACTGCGAGAGCGATGTTGACGCGCGCGGATTTGCGGCTG 660
QY 991 GCGGTGTTGGGCGACCTGCTATACCAACCGCGGCTTCCAGAGAGAGTTCGCAAAAGCGAAG 1050

PD 28-NOV-1996.
XX
XX PF 24-MAY-1996; 96WO-JP001402.
XX
PR 25-MAY-1995; 95JP-00149781.
XX PR 26-MAR-1996; 96JP-00094680.
XX
XX PA (AJIN) AJINOMOTO CO INC.
XX
XX PI Mihara Y, Utogawa T, Yamada H, Asano Y;
XX
XX WPI; 1997-021215/02.
DR P-PSDB; AAW06462.
XX
XX PT Efficient production of nucleoside 5'-phosphate - by reaction of a
XX nucleoside with a phosphoric acid donor in the presence of an acid
XX phosphatase.
XX
XX PS Example 8; Page 50-51; 95pp; Japanese.
XX
XX CC The present sequence encodes the Morganella morganii NCIMB 10466 acid
XX phosphatase (AP), which can be used to produce a nucleoside 5'-phosphate
XX ester from the corresponding nucleoside when a phosphate donor, e.g. poly
XX -, phenyl- or carbamyl-phosphoric acid, is reacted in its presence at pH
XX 3.0 to 5.5. The PA can be used for the economic and efficient production
XX of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals
XX and intermediates for pharmaceuticals
XX
XX SQ Sequence 750 BP; 198 A; 194 C; 198 G; 160 T; 0 U; 0 Other;
Query Match 34.4%; Score 422; DB 2; Length 750;
Best Local Similarity 72.7%; Pred. No. 6.9e-122;
Matches 545; Conservative 0; Mismatches 205; Indels 0; Gaps 0;
331 ATGAAAAACGTTCTGGCAGTTGTTTGGCGATGTTCTCTCTCAGGCCCTGGCG 390
Db 1 ATGAAAGAGAATATTATCCGGTGTCTGTGTTCTCACTGTTTCCCTTTCCGCGCTGGCC 60
391 CTGGTGTCTACCGGCAACGACACTACCGAAACCGGATCTCTACTACCTCAAGAACAGT 450
Db 61 GCGATCCCGGGGCAACGATGCCACCAACGCGGATTTATATCTGAAATGAA 120
451 GAAGCCATTAAACAGCTGCGCTGTTTGGCCGACCAACCGCGGTTGCGTCCATTCGTTTT 510
Db 121 CAGGCTATCGACAGCTGAACTGTTACCGCCACCGCCGGAAGTCGGCAGTATTCAGTTT 180
511 CTCACGATCAGCGCATGTATGAACAGGGCGGCTGCTGGCGAACACCGAAGCGGTAG 570
Db 181 TAAATGATCAGGCAATGTATGAGAAAGCCGTATGCTGCGCAATACCGAGCGGAA 240
571 CTGGCGGGAAGATGCAAACTGAGCAGTGTGGGGGTGGCGAAATGCTTTCTCGGCGG 630
Db 241 CAGGACAGGAGATGCTGACCTGGCGCGAGGGGTGTGGCAACCGCATTTTCAGGGCA 300
631 TTTGTAGCCGATCAGCGAAAGAGCGCCCGCGCTGCTCATTAATTAATTCACCAATATG 690
Db 301 TTGGCTATCCGATAACCGAAAGAACTCTCGGAGCTGTATAAATCTGTGACCAATATG 360
691 ATTGAGGAGCGGGGATCTGGGACCGCGACGCGGCAAGATCACTATATGCGATTCCT 750
Db 361 ATTGAGGAGCGGGGATCTTCCACCGCTCTCCGCAAGAACATTTACATGGCGATCCGG 420
751 CGTTTCGGGTTTATGGGTTCTCTACCTGTAATACCAACGAGGAGCAAACTGTCCAAA 810
Db 421 CGTTTGGTTTACGGCACAGAACCTGTATACCAAGATCAGAAAACTCTCCACC 480
811 AATGCTCTTATTCGTCGGGATACCTTATCGGCTGGGCTATCGGCTGGTGTCTGGCA 870
Db 481 AACGGATCTTACCCGTCAGTCTATCGCTGGGCAACCGCACTGTGTCTGGCG 540
871 GAGATCAACCTTCAGCGCCAGACGATCTCTCAACCGGTTTATGAGCTGGCCAGAGC 930
Db 541 GAAGTGAACCCGCAATCAGGATGCGATTC-TGAAACGGGGTTATCAGCTCGGACAGAGC 600

QY 931 CGGGTGAATTTGGGCTACCACTGGCAGAGTGATGTGGATCCCGCGGGTAGTGGATCT 990
Db 601 CGGGTGAATTTGGGCTATCACTGGCAGAGTGATGTGGATCCCGCGGGTAGTGGATCT 660
QY 991 GCCGTGTGGGACCCCTGCATACCAACCCGGGCTTCCAGCAGAGTTGCAGAAAGCGAAG 1050
Db 661 GCCGTGTGGGACATTAATTCGATCCGATCCGATTCAGGCGCAGTTAGCGAAAGCCAA 720
QY 1051 GCCGAATTCGCCAGCATCAGAGAAATRA 1080
Db 721 CAGGAATTTGCACAAAATCAGCAAAATRA 750
RESULT 11
AAV43045
ID AAV43045 standard; DNA; 750 BP.
XX
XX AC AAV43045;
XX
XX DT 21-OCT-1998 (first entry)
XX
XX DE DNA encoding an acid phosphatase enzyme.
XX
XX KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
XX intermediate; ds.
XX
XX OS Morganella morganii.
XX
XX FH Key Location/Qualifiers
FT CDS 1..750
FT sig_peptide 1..60 /*tag= a
FT mat_peptide 61..747 /*tag= b
FT /*tag= c
XX
XX PN EP857788-A2.
XX
XX PD 12-AUG-1998.
XX
XX PP 20-NOV-1997; 97EP-00309365.
XX
XX PR 21-NOV-1996; 96JP-00311103.
XX PR 18-JUN-1997; 97JP-00161674.
XX
XX PA (AJIN) AJINOMOTO CO INC.
XX
XX PI Mihara Y, Utogawa T, Yamada H, Asano Y;
XX
XX WPI; 1998-416010/36.
DR P-PSDB; AAW71028.
XX
XX PT Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
XX with phosphate donor in presence of acid phosphatase - used as seasonings
XX or pharmaceutical intermediates.
XX
XX PS Example 8; Page 30-31; 83pp; English.
XX
XX CC The present sequence encodes an acid phosphatase enzyme. The
XX specification describes a method for the preparation of nucleoside 5'-
XX phosphate esters. The method comprises reacting a nucleoside with a
XX phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
XX has been altered to increase its affinity for the nucleoside and/or to
XX increase its thermal stability, or in the presence of a microorganism
XX that has been transformed with recombinant DNA containing a gene coding
XX for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
XX seasonings or pharmaceuticals or as intermediates for them
XX
XX SQ Sequence 750 BP; 198 A; 194 C; 198 G; 160 T; 0 U; 0 Other;
Query Match 34.4%; Score 422; DB 2; Length 750;
Best Local Similarity 72.7%; Pred. No. 6.9e-122;

Matches 545; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 331 ATGAAAACGGTCTTCCAGTGTGTTGCGCATGTTCTCTCAGGCGCTGGCG 390
DB 1 ATGAGAAGAAATATATCGCGGTGTCGTTCTCACTGTTTCCCTTTCGCGCTGGCC 60

QY 391 CTGGTCCGTACCGGCAACGACATACACCAAAACCGGATCTCTACTACCTCAAGAACGT 450
DB 61 GCATCCCGGGGCAACGATGACACCAACGCGGATTTATATATCTGAAAAATGAA 120

QY 451 GAAGCCATTAAACGCTGCGCTGTTCCGCGACCAACGCGGTGGCTCCATTGCGTTT 510
DB 121 CAGGCTATCAGACGCTGAACTGTACCGCCACCGCGGAAAGTCGCGCATTTCACTT 180

QY 511 CTCAAGATCAGCCCATGTATGACAGCGGCGCTGTCGCAACCGCAACCGGTAAG 570
DB 181 TTAATGATCAGCAATGTATGAAAGGCGGTATGCTGCGCAATCCGAGCGGAAAA 240

QY 571 CTGCGCGGGAAGATGCAAACTGAGCAGTGGCGGGTGGCGAATGCTTCTCCGCGCG 630
DB 241 CAGGCAAGCAGATGTGACCTGGCGCAGCGGTGTGGCAACCGCATTTTCAGGGCA 300

QY 631 TTGGTAGCCGATACCGAAAAGACGCGCCCGCTGCAATAAATTAATGACCAATG 690
DB 301 TTGGGTATCCGATAACCGAAAAGACTCTCCGAGCTGTATTAACCTGCTGACCAATG 360

QY 691 ATTGAGGACCGCGGATCTGCGACCGCGCAGCGCGAAGATCACTATATGCGATTGCT 750
DB 361 ATTGAGGATCCCGGTGATCTTGGCACCGCTCGCCAAAGCAATTAATGCGATCCGG 420

QY 751 CCGTTCGCTTTATGGGGTCTCTACTCTGTAATACCAACCGAGCAGCAAACTGTCCAAA 810
DB 421 CCGTTGCGTTTACGCAAGAACTGTATTAACCAAGATCAGAAAAAATCTCCACC 480

QY 811 AATGCTCTTATCCGTCGCGGCAATCTCTATCGGCTGGGCTACTGCGCTGGTGGCA 870
DB 481 AACGGATCTTACCGCTCAGGCTATACCTCTATCGGCTGGGCAACCGCACTGGTGGCG 540

QY 871 GAGATCAACCTCAGCGCGAAGCAGATCTCTGAAACGCGGTTATGAGCTGGGCGCAGC 930
DB 541 GAAGTAGCCCGCAATCAGATGCGATTTGGAACGGGTTATCAGCTCGACAGC 600

QY 931 CCGGTGATTTGCGCTACCTGCGCAGATGATGAGATGCGCGCGGTGATGCGATCT 990
DB 601 CCGGTGATTTGCGCTATCACTGCGCAGATGATGAGATGCGCGCGGATTTGCGTTCA 660

QY 991 CCGGTTGCGGACCTGCGATACCAACCGCGGTTCCAGCAGCAGTTGCAAGAGCAG 1050
DB 661 CCGGCTGCGCGCATTAATTCGATCCGCAATTTCCAGCGCGAGTTAGCGAAGCCAAA 720

QY 1051 GCGAATTCGCCAGCATCAGAGAAATAA 1080
DB 721 CAGGAATTCGCAAAAATCAGAAATAA 750

RESULT 12

AAT45012

ID AAT45012 standard; DNA; 747 BP.

XX AAT45012;

AC AAT45012;

XX

DE 13-AUG-1997 (first entry)

XX

DE Providencia stuartii ATCC 29851 acid phosphatase DNA.

XX

KW ATCC 29851; acid phosphatase; production; nucleoside; 5'-phosphate;

XX

KW ester; condiment; pharmaceutical; intermediate; ds.

XX

OS Providencia stuartii.

XX

FH Key Location/Qualifiers

FT CDS 1..747

FT /*tag= a

/product= "acid_phosphatase"

WO9637603-A1.

XX

PD 28-NOV-1996.

XX

XX 24-MAY-1996; 96WO-JP001402.

XX

XX 25-MAY-1995; 95JP-00149781.

XX

XX 26-MAR-1996; 96JP-00094680.

XX

XX (AJIN) AJINOMOTO CO INC.

XX

XX Mihara Y, Utagawa T, Yamada H, Asano Y;

XX

XX WPI; 1997-021215/02.

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XX P-PSDB; AAM06457.

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Efficient production of nucleoside 5'-phosphate - by reaction of a nucleoside with a phosphoric acid donor in the presence of an acid phosphatase.

Example 23; Page 63-65; 95pp; Japanese.

The present sequence encodes the Providencia stuartii ATCC 29851 acid phosphatase (AP), which can be used to produce a nucleoside 5'-phosphate ester from the corresponding nucleoside when a phosphate donor, e.g. poly-phenyl- or carbamyl-phosphoric acid, is reacted in its presence at pH 3.0 to 5.5. The PA can be used for the economic and efficient production of nucleoside 5'-phosphate esters for use as condiments, pharmaceuticals and intermediates for pharmaceuticals

Query Match 29.2%; Score 357.4; DB 2; Length 747;

Best Local Similarity 67.6%; Pred. No. 1.5e-101;

Matches 502; Conservative 0; Mismatches 241; Indels 0; Gaps 0;

QY 331 ATGAAAACGGTCTTCCAGTGTGTTTCCGCGATGTTCTCTCTCAGGCGCTGGCG 390

DB 1 ATGAAAACCTATTAGCAGTATTCTGCGCAGGGCTTTGTTTCAACAGTGTATTGCG 60

QY 391 CTGTCCTCTACCGCAAGCAGTCTACACGAAACCGGATCTCTACTACTCAAGACAGT 450

DB 61 GCGATCCCTCCCGCAATGATGTGCAAACTAAACCCGATCTTATTTATTTAAAAACATCA 120

QY 451 GAAGCCATTAAACGCTTCCGCGCTGTTCCGCGACCAACCGCGGTGGCTCCATTGCGTTT 510

DB 121 CAGCTATTGATAGTTTAGCGTTTATTTGCGCCACCACTGAAGTGGGAGTATCTTATTT 180

QY 511 CTCAACGATCAGGCGCATGTATGAAACAGGCGCTCTGTCGCAACACCGAACCGGTAAG 570

DB 181 TTAACGACCAAGCATGTATGAAAAGGCGCTTTATTCGAAATATCTGCGCTGAGAA 240

QY 571 CTGCGCGGAGATGCAAACTGAGCAGTGGCGGGTGGCGAATGCTTCTCCGCGCG 630

DB 241 CAAGCCGCTAGGATGCTGATCTGCGCTGCGGGCGGTGTGCGAAGCGCATTTCTGAGCT 300

QY 631 TTTGCTAGCCCGATCACCGAAAAGACGCCCCCGGCTGCAATAAATTAATGACCAATATG 690

DB 301 TTTGTTATCCATTCGAAAAGATGCGGCTGAAATTCATTAATTCGCTGAGCAATATG 360

QY 691 ATTGAGGACCGCGGATCTGCGCAACCGCGAGCGGAAAGATCACTATATGCGATTGCT 750

DB 361 ATTGAGGATCCCGGTGATTTAGCAACTGCTCTAGCAAAAGAGAAATATCATGCGCATTCGT 420

QY 751 CCGTTCCGTTTATGGGCTCTCTACCTGTAATACCCGAGCAGGCAAACTGTCCAAA 810

DB 421 CCAATTGCGTTCTACGGTGTGCTACCTGTATTAACCAAGAAATATCTTAAAG 480

QY 811 AATGCTCTTATCCGTCGCGGCACTCTATTCGCTGGGCTACTGCGCTGGTGGCA 870

DB 481 AATGCTCTTATCCCTCTGGAACACACCGCAATTCGCTGGGCACTCTGCTATGTGCA 540

QY 871 GAGATCAACCTCAGCGCCAGACAGATCCTGAAACGGGTTATGAGTGGCCAGAGC 930
 DB 541 GAAATTAACCCAGAGAAACCAAGATAAAATTTAAACGGTGGTTATGAACTGGCCRAAGC 600
 QY 931 CGGTGATTTTCGGGTACCACTGGCAGAGTGTATGTGGATGCCGCGGGTGTAGTGGATCT 990
 DB 601 CGAGTCATCTGTGGTTACCAATGGCAAGTGTATGTGAGTCAGTCGTATCGTTGCATCG 660
 QY 991 GCCGTTGTGGGACCTCGATACCAACCGGGGTTCCAGCAGCACTTCGAGAAAGGAG 1050
 DB 661 GGTGGGTAGCAACTTTACACTCCAACTCGAATTTCAAAAACAGTTACAAAAGCCAAA 720
 QY 1051 GCCGAATTCGCCAGCATCAGAA 1073
 DB 721 GACGAATTTGCTAAACTGAAAA 743
 RESULT 13
 ID AAV43059 standard; DNA; 747 BP.
 XX AC AAV43059;
 XX DT 21-OCT-1998 (first entry)
 XX DE DNA encoding an acid phosphatase enzyme.
 XX KW Acid phosphatase; preparation; nucleoside 5'-phosphate ester; seasoning;
 XX KW intermediate; ds.
 XX OS Providencia stuartii.
 XX FH Key Location/Qualifiers
 XX FT 1..747
 XX FT /*tag= a
 XX EP857788-A2.
 XX PD 12-AUG-1998.
 XX PF 20-NOV-1997; 97EP-00309365.
 XX PR 21-NOV-1996; 96JP-00311103.
 XX PR 18-JUN-1997; 97CP-00161674.
 XX PA (AJTN) AJTNMOTO CO INC.
 XX PI Mihara Y, Utogawa T, Yamada H, Asano Y;
 XX WP: 1998-416010/36.
 XX P-PSDB; AAW71230.
 XX Preparation of nucleoside 5'-phosphates comprises reacting nucleoside
 PT with phosphate donor in presence of acid phosphatase - used as seasonings
 PT or pharmaceutical intermediates.
 XX Example 23; Page 40-41; 83pp; English.
 XX The present sequence encodes an acid phosphatase enzyme. The
 CC specification describes a method for the preparation of nucleoside 5'-
 CC phosphate esters. The method comprises reacting a nucleoside with a
 CC phosphate donor at pH 3.0-5.5 in the presence of an acid phosphatase that
 CC has been altered to increase its affinity for the nucleoside and/or to
 CC increase its thermal stability, or in the presence of a microorganism
 CC that has been transformed with recombinant DNA containing a gene coding
 CC for such an acid phosphatase. Nucleoside 5'-phosphates are useful as
 CC seasonings or pharmaceuticals or as intermediates for them
 XX SQ Sequence 747 BP; 226 A; 156 C; 166 G; 199 T; 0 U; 0 Other;
 Query Match 29.2%; Score 357.4; DB 2; Length 747;
 Best Local Similarity 67.6%; Pred. No. 1.5e-101;

Matches 502; Conservative 0; Mismatches 241; Indels 0; Gaps 0;
 QY 331 ATGAAAAAGCGTTCTGCGAGTTGTTTGTGCGCATTTCTCTCTCTCAGGCGCTGGCG 390
 DB 1 ATGAAAAAATATTATAGCAGTATCTGCGCAGGGGCTTTTGTTCACACAGTGTATTGCG 60
 QY 391 CTGGTCGCTACCGGCAACGACACTACACGAAACCGGATCTCTACTACTCAAGAACAGT 452
 DB 61 GCGATCCCTCCCGCAATGATGTGACAACTAAACCCGATCTTTATTTTAAAAAACCTCA 120
 QY 451 GAAGCCATTAAAGCCTGGCGCTGTTCGCCACACCGCGTGGGCTCCATTGCGTTT 510
 DB 121 CAGGCTATTGATAGTTAGCGTTATTGCCGCCACACCTGAGTGGGCGATCTATTATT 180
 QY 511 CTCAACGATCAGGCCATGTATGAAACAGGGGCGCTGCTGCGCAACACCGACCGGTAG 570
 DB 181 TTAAACGACCAAGCGATGTATGAAAAAGCGCTTTATTTCGAAATACTGAGCGTGAGAA 240
 QY 571 CTGGCGGCGGAAGATGCAAACTGAGCAGTGGCGGGTGGCGAATCTTTCTCCGGCGG 630
 DB 241 CAAGCGCTAAGGATGCTGATCTGGCTGGCGGGGCTTTGCGAACGCACTTTCTGAAGCT 300
 QY 631 TTTGGTAGCCCGATCACCGAAGAACGCGCCCGCGCTGCATAAATTTACTGACCAATATG 690
 DB 301 TTTGGTTATCCCATTACCGAAGAGGATGCGCCCTGAAATTCATAAATTTCTGACGATATG 360
 QY 691 ATTGAGGACGCGGGGATCTGGCGACCCGCGAGCGCGAAGATCACTATATGCGCATTCGT 750
 DB 361 ATTGAGATGCGGGGATTTAGCAACTGCTCAGCCAAAGAGAAATACATGCGCATTCGT 420
 QY 751 CCGTTGCGGTTTTATGGGGTCTCTACTGTATATACCGAGCAGGACGAACTGTCCAAA 810
 DB 421 CCATTTGCGTTCTACGCTGTGCTACCTGTAAACACGAAAGATCAGGACAAATTTATCTAAG 480
 QY 811 AATGCTCTTATCGTCCGCGCATCTCTATCGGCTGGGCTACTCGCTGGTGTGCTGCA 870
 DB 481 AATGGCTCTTATCTCTCTGACACACCGCAATTTGGCTGGCATCTGCATCTGTTATGCA 540
 QY 871 GAGATCAACCCCTCAGCGCCAGAACGAGATCTCTCAACCGGGTTATGAGTGGCGCCAGAGC 930
 DB 541 GAAATTAACCCAGAAAAACCAAGATAAAATTTTAAACGGTGGTTATGAACTGGCCRAAGC 600
 QY 931 CGGTGATTTTCGGGTACCACTGGCAGAGTGTATGTGGATGCCGCGGGTGTAGTGGATCT 990
 DB 601 CGAGTCATCTGTGGTTACCAATGGCAAGTGTATGTGAGTCAGTCGTATCGTTGCATCG 660
 QY 991 GCGTTGTGGCGACCTCGATACCAACCGGGGCTTCAGCAGCACTTCGAGAAAGGAG 1050
 DB 661 GGTGGGTAGCAACTTTACACTCCAACTCGAATTTCAAAAACAGTTACAAAAGCCAAA 720
 QY 1051 GCCGAATTCGCCAGCATCAGAA 1073
 DB 721 GACGAATTTGCTAAACTGAAAA 743

RESULT 14

AAT45009
 ID AAT45009 standard; DNA; 735 BP.

XX AC AAT45009;

XX DT 13-AUG-1997 (first entry)

XX DE Serratia marcescens IAM 13540 acid phosphatase DNA.

XX KW IAM 13540; acid phosphatase; production; nucleoside; 5'-phosphate; ester;
 XX KW condiment; pharmaceutical; intermediate; ds.

XX OS Serratia marcescens.

XX FH Key Location/Qualifiers

XX FT 1..735

XX FT /*tag= a

Query Match 24.9%; Score 304.6; DB 2; Length 735;
Best Local Similarity 63.7%; Pred. No. 6.4e-85; Mismatches 264; Indels 0; Gaps 0;
Matches 463; Conservative 0;

QY 351 AGTTTGTTCGGCATTTCTCTCTCAGGCCCTGGCGCTGGTGGCTACCGGCAACGA 410
DB |||||
DB 9 AATATTATTAGCCACATTAAAGCTGGCGCGGTTGACGCGAGTTTCTCTTGGCGCCAAAGA 68
QY 411 CACTACCAAGAACCGGATCTCTACTACTCAAGACAGTGAAGCCATTAAAGCCTGGC 470
DB |||||
DB 69 TGTCACTACCCACCTCGAGGTTTATTCTTCTGCAAGAAATCACAGTCCATCGACAGCCTGGC 128
QY 471 GCTGTTGGCGCCACACCGCGGCTGGGCTCCATTGGGTTTCTCAGCATCAGGCCATGTA 530
DB |||||
DB 129 ACTATTGGCGCGCGCGCGGCGGATGACAGCATTTGATTTCTTGATGACAGCGCAATA 188
QY 531 TGAACAGGGGCGGCTGCTCGCAACACCGAAGCGGTAAGCTGGCGCGGGAAGATCAAA 590
DB |||||
DB 189 CGAGCGCGGGAATAAGTGGCAATCTCCGCGTGCAAGCAGGCTTATGATGACGCCA 248
QY 591 CTTGAGCAGTGGCGGCTGGGAATCTTCTCCGCGGCTTGGTAGCCCGATCACCGA 650
DB |||||
DB 249 CGTTGCGGGGAGCGGCTTGGCGCGCATTTTCCAAACGCGCTTGGGCTAGAAATAGCCCA 308
QY 651 AAAAGAGCGCGCGGCTGCATAAATTACTGACCAATATGATTGAGGAGCGCGGGATCT 710
DB |||||
DB 309 ACGGAAGCGCGGAGCTGTTTAAGCTGGTATGAAATGCGTGAAGAGCGCGGCGATTT 368
QY 711 GCGGACCGCGAGCGGGAAGATCACTATATGGCATTCGTTCCGTTCCGTTTTATGGGT 770
DB |||||
DB 369 GCGGACCGCGAGCGGCAAAATCACTATATGGCATTCGCCCCCTTGGGTTTTATAACGA 428
QY 771 CTTTACCTGTAATACACGAGGAGGACAACTGTCCAAATGCGCTCTATCCGTCGCG 830
DB |||||
DB 429 AGCGACCTCCGACCGGACGAAAGAACCCCTGTGAAAGACGGTTCTTACCCCTTCGCG 488
QY 831 GCATACCTCTATCGGCTGGGCTACTCGGCTGGTGGTGGAGAGATCAACCCCTCAGCGCCA 890
DB |||||
DB 489 CCATACCAACCTCGGCTGGCGGACCGGCTGGTGGTGGTGAATCAACCCCGCAGGCA 548
QY 891 GAACGAGATCCTGAACACGCGGTTATGAGCTGGGCGCAGAGCGGGTGAATTTGGGCTACCA 950
DB |||||
DB 549 GGGTGAATCCTCGAGCGGGCTATGATATGGGCCAAAGCCGGGTTATCTGCGGTTATCA 608
QY 951 CTGGCAGAGTGTGGATGCGCGCGGCTAGTGGGATCTGCGGTTGTGGGACCCCTGCA 1010
DB |||||
DB 609 CTGGCAAGCGAGCTGACTCGCGCGGCTATGGCGGCTCGGCCATGGTGGCGGTTTGA 668
QY 1011 TACCAACCGCGGTTCCAGCAGAGTTGCAAGAGCGAGGCGCGAATTCGCCCAGCATCA 1070
DB |||||
DB 669 TGGCGAACCTCACTTCGCGCGCCAGCTGCAAGAGCCAGAGCAATTCACCGGCTGAA 728
QY 1071 GAAGAAA 1077
DB |||||
DB 729 AAAGTAA 735

Search completed: June 4, 2004, 19:01:36
Job time : 416 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 19:59:11 ; Search time 432 Seconds
(without alignments)
12936.216 Million cell updates/sec

Title: US-09-807-990-1

Perfect score: 1225

Sequence: 1 ctgcaggcgaaggcaatgt.....taagatcatgtgcggttaac 1225

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 5991872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:*

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- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	44.6	3.6	62909	13	US-10-672-787-32
C 2	39.6	3.2	1830	13	US-10-672-787-32
C 3	37.6	3.1	1332	15	US-10-156-761-25435
C 4	37.6	3.1	9025608	15	US-10-156-761-2570
C 5	37.4	3.1	1695	13	US-10-342-887-1167
C 6	37.4	3.1	1695	13	US-10-172-118-1167
C 7	37.4	3.1	2270	15	US-10-393-590-61
C 8	37.4	3.1	2270	15	US-10-393-567-61
C 9	37.4	3.1	2270	15	US-10-394-087-61
C 10	37.4	3.1	2310	9	US-09-919-172-34
C 11	37.4	3.1	2310	9	US-09-974-298-42
C 12	37.4	3.1	2310	13	US-10-116-802-210
C 13	37	3.0	639	13	US-10-027-632-279124
C 14	37	3.0	639	13	US-10-027-632-279125

C 15	37	3.0	639	16	US-10-027-632-279124	Sequence 279124,
C 16	37	3.0	639	16	US-10-027-632-279125	Sequence 279125,
C 17	37	3.0	1866	9	US-09-738-626-1317	Sequence 1317, Ap
C 18	37	3.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
C 19	36.8	3.0	945	16	US-10-084-846A-71	Sequence 71, Appl
C 20	36.8	3.0	59816	16	US-10-084-846A-1	Sequence 1, Appli
C 21	36.8	3.0	59816	16	US-10-084-846A-2	Sequence 2, Appli
C 22	36.8	3.0	68750	14	US-10-014-717-1	Sequence 1, Appli
C 23	36.8	3.0	71989	13	US-09-727-889-2	Sequence 2, Appli
C 24	36.4	3.0	354	15	US-10-156-761-5162	Sequence 5162, Ap
C 25	36.4	3.0	669	16	US-10-260-238-5254	Sequence 5254, Ap
C 26	36.4	3.0	9025608	15	US-10-156-761-1	Sequence 1, Appli
C 27	36.2	3.0	2229	15	US-10-156-761-6567	Sequence 6567, Ap
C 28	36	2.9	867	15	US-10-156-761-1437	Sequence 1437, Ap
C 29	36	2.9	2000	9	US-09-887-576-333	Sequence 333, App
C 30	35.8	2.9	732	13	US-10-282-122A-14920	Sequence 14920, A
C 31	35.8	2.9	1017	13	US-10-440-503-29	Sequence 29, Appl
C 32	35.8	2.9	1017	13	US-10-461-925-29	Sequence 29, Appl
C 33	35.8	2.9	1017	15	US-10-146-772-29	Sequence 29, Appl
C 34	35.8	2.9	1017	16	US-10-241-742-29	Sequence 29, Appl
C 35	35.8	2.9	1017	16	US-10-440-523-29	Sequence 29, Appl
C 36	35.6	2.9	888	9	US-09-974-300-1129	Sequence 1129, Ap
C 37	35.2	2.9	536	17	US-10-338-110-119	Sequence 119, App
C 38	35	2.9	586	15	US-10-029-386-12315	Sequence 12315, A
C 39	35	2.9	645	15	US-10-207-655-417	Sequence 417, App
C 40	34.6	2.8	802	15	US-10-184-644-312	Sequence 312, App
C 41	34.6	2.8	802	15	US-10-184-634-312	Sequence 312, App
C 42	34.4	2.8	1404	13	US-10-282-122A-26411	Sequence 26411, A
C 43	34.4	2.8	1407	13	US-10-282-122A-28207	Sequence 28207, A
C 44	34.4	2.8	1971	16	US-10-369-493-39994	Sequence 39994, A
C 45	34.4	2.8	1995	16	US-10-369-493-39628	Sequence 39628, A

ALIGNMENTS

RESULT 1

US-10-672-787-32/c
; Sequence 32, Application US/10672787
; Publication No. US20040067554A1
; GENERAL INFORMATION:
; APPLICANT: LAGACE, Robert, E.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BERG, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: ELITRA.025C1
; CURRENT APPLICATION NUMBER: US/10/672,787
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 09/596,002
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 32
; LENGTH: 62909
; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
; US-10-672-787-32

Query Match	3.6%	Score	44.6	DB	13	Length	62909
Best Local Similarity	53.8%	Pred. No.	0.011				
Matches	92	Conservative	0	Mismatches	79	Indels	0
						Gaps	0
QY	793	CAGGACAAACTGTCACAAATGGCTTTATTCCTCGGGGATACCTTATTCGGTGGGCT	852				
DB	40121	CAAGGCAGAGAAAGAAAATTCATCTTATCCAAAGTGGGATACCTCCAAATGGTTTGGT	40062				
QY	853	ACTGCGTGGTGTGGCAGAGATCAACCTCAGCGCCAGACGAGATCCTGAAACGGGT	912				
DB	40061	CAAGCGGTGTGTGATGGCGATTCCTTCCTGAGCAGGTCAAGAGATTTCTCTCGTCA	40002				
QY	913	TATGAGCTGGCGCAGAGCGGGTATTTCGGCTTACCTACCTGGCAGAGTGAT	963				
DB	40001	TTCCAGTATGGAGAAAGCCGAGTCATGTGGGTGTGATTTTCCACAGAT	39951				

RESULT 2

US-10-282-122A-25435
; Sequence 25435, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Chlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A US/10/282,122A
; CURRENT APPLICATION NUMBER: 2003-02-20
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25435
; LENGTH: 1833
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-282-122A-25435

Query Match 3.2%; Score 39.6; DB 13; Length 1830;
Best Local Similarity 48.9%; Pred. No. 0.064;
Matches 136; Conservative 0; Mismatches 139; Indels 3; Gaps 1;
QY 390 GCTGTCCTACCGCAACGACACTACACGAAACCGGATCTCTACTACTCAAGAACAG 449
DB 225 GGTGCTCTGCGCCGAGGACGAGACCGGAGCTGTGGAGCTCTCGACCTGACCTACG 284
QY 450 TGAAGCCATTAAACAGCTGGCGCTGTTCGCGCACACCGCGGTGGGCTCCATTGCGGT 509
DB 285 CGAGGACGAGGACACCGAGGAGGACCTGACAGCGCGCGCGGTGGTGAACGCTATGG 344
QY 510 TCTCAAGATCAGGCCATGTATACAGGGGCGCTGTGCGACACCGACGACGCGTAA 569
DB 345 TCAGCTGACACCGGTAAGACGCGCTGCTGGACACGATCCGTAAGGCCAACGCTCGGA 404
QY 570 GCTGCGCGGGAAGATGCAAACTCAGCAGTGGCGGGGT---GGGGAATGCTTTCTCCGG 626
DB 405 GCGGAGCGCGGCGATCACCACACATCGGCGCTACAGGTGACCGCTGACGACGA 464
QY 627 CCGCTTTGTAGCCCGATCACCGAAAAAGACGCCCGG 664

DB 465 CGGGGTGGAGCGCCCGATCACTTCACTGACACCCCGG 502

RESULT 3

US-10-156-761-2570
; Sequence 2570, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2570
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1332)
US-10-156-761-2570

Query Match 3.1%; Score 37.6; DB 15; Length 1332;

Best Local Similarity 51.8%; Pred. No. 0.26; Indels 0; Gaps 0;
Matches 85; Conservative 0; Mismatches 79;

QY 857 CGCTGCTGTCGACAGATCAACCTCAGCGCCAGACGAGATCTCTGAACCGGTATG 916
DB 479 CGATGGCGCTGACCGCGAGACATCGCGTACAGACGGCTTCGGACCGTTGCGCGCG 538
QY 917 AGCTGGCGCAGACCGCGGTGATTTCGGCTACCATCGCAGAGTGTGTGGATGCGCGC 976
DB 539 AGTCTACCGGCTGCGGTGCGGTACGCTACCGCTGCTACCGCGCCGCGAGACGCG 598
QY 977 GGTAGTGGGATCTGCGCTGTGGCGACCTCATACCAACCG 1020
DB 599 GTGCGGAGGCGCTCGCGCGGATCGACATGATCAACAGCAG 642

RESULT 4

US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1

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; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-0-156-761-1

Query Match      3.1%; Score 37.6; DB 15; Length 9025608;
Best Local Similarity 51.8%; Pred. No. 63; Mismatches 79; Indels 0; Gaps 0;
Matches 85; Conservative 0;

QY 857 CGCTGGTGTGGCAGAGATCAACCTTCAGCGCCAGAACCGAGATCTCTGAACCGGGTTATG 916
DB 3175941 CGATGGCGCTGACCGCGAAGACATGCCGTACAAGAACGGCTTCGGACCGTTCGGCCCG 3176000

QY 917 AGCTGGGCGAGACCGCGGTGATTTGGGCTACCATCGCAGAGTATGTGGATGCGGCGC 976
DB 3176001 AGGTCTACCGGGTGGCGGTGGCGTACCGCTACCGTGGCTGACCGCGCCGCGAGAACGCG 3176060

QY 977 GGGTAGTCGGATCTCCGTTGGCGGACCTCATACCAACCCG 1020
DB 3176061 GTGCGGAGGCTCCGCCAGCGGCTGACATGATCAACAGCAG 3176104

RESULT 5
US-10-342-887-1167
; Sequence 1167, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1167
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1167

Query Match      3.1%; Score 37.4; DB 13; Length 1695;
Best Local Similarity 49.2%; Pred. No. 0.35;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 891 CTCAGCGCCAGAACAGATCTCTGAACCGGGTTATGATGGCCAGAGCCGGGTGATT 940
DB 1145 CTGAGATCAACCGCATGATCCAGAGGCTGAGATCTGAGATCGACCAAGAGCAGT 1204

QY 941 GCGGCTACCACTGGCAGAGTGTGGATCGCGGGGTAGTGGATCTGCCGTTGTGG 1000
DB 1205 GCGCAACCTGCGAGCGGCCCATCTGCTGATGCTGAGCAGCGTGGGGAGATGGCCCTCAGG 1264

QY 1001 CGACCTCTGCATACCAACCGCGGTTCCAGCAGCAGTTGCAGAAAGCGAAGCCGAATTGG 1060
DB 1265 ATGCCAAGAACCAAGCTGTGAAGGGCTGGAGGATGCCCTGCAGAAAGGCCAAGCAGGACCTGG 1324

QY 1061 CCCAGCATCAGAAGAAATA 1079
DB 1325 CCCGGCTGCTGAAGGAGTA 1343

RESULT 6
US-10-393-590-61
; Sequence 61, Application US/10393590
; Publication No. US20030190656A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: BREAST CANCER PROGNASTIC PORTFOLIO
; FILE REFERENCE: CDS 268 US NP
; CURRENT APPLICATION NUMBER: US/10/393,590
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,789
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 61
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: human
US-10-393-590-61
```

```
DB 1325 CCCGGCTGCTGAAGGAGTA 1343

RESULT 6
US-10-172-118-1167
; Sequence 1167, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1167
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_005554
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1167

Query Match      3.1%; Score 37.4; DB 13; Length 1695;
Best Local Similarity 49.2%; Pred. No. 0.35;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 881 CTCAGCGCCAGAACAGATCTCTGAACCGGGTTATGATGGCCAGAGCCGGGTGATT 940
DB 1145 CTGAGATCAACCGCATGATCCAGAGGCTGAGATCTGAGATCGACCAAGAGCAGT 1204

QY 941 GCGGCTACCACTGGCAGAGTGTGGATCGCGGGGTAGTGGATCTGCCGTTGTGG 1000
DB 1205 GCGCAACCTGCGAGCGGCCCATCTGCTGATGCTGAGCAGCGTGGGGAGATGGCCCTCAGG 1264

QY 1001 CGACCTCTGCATACCAACCGCGGTTCCAGCAGCAGTTGCAGAAAGCGAAGCCGAATTGG 1060
DB 1265 ATGCCAAGAACCAAGCTGTGAAGGGCTGGAGGATGCCCTGCAGAAAGGCCAAGCAGGACCTGG 1324

QY 1061 CCCAGCATCAGAAGAAATA 1079
DB 1325 CCCGGCTGCTGAAGGAGTA 1343

RESULT 7
US-10-393-590-61
; Sequence 61, Application US/10393590
; Publication No. US20030190656A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: BREAST CANCER PROGNASTIC PORTFOLIO
; FILE REFERENCE: CDS 268 US NP
; CURRENT APPLICATION NUMBER: US/10/393,590
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,789
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 61
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: human
US-10-393-590-61
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Query Match 3.1%; Score 37.4; DB 15; Length 2270;
Best Local Similarity 49.2%; Pred. No. 0.42;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 881 CTCAGGCCAGAACGAGATCTCTGAACCGCGTTATGAGCTGGCCAGAGCCGGTGATTT 940
DB 1193 CTGAGATCAACCGCATCCAGAGGCTGAGATCTGAGATCGACACGTCAGAGCAGT 1252
QY 941 GCGGCTACCACTGGCAGAGTGTGATGTCGCCGGGTAGTGGATCTGCCGTGTGG 1000
DB 1253 GCGCCAACTGCAGCGCGCCATTGCTGATCTGAGCAGCGTGGGAGAGGCCCTCAAG 1312
QY 1001 CGACCTGTCATACCAACCGCGTTCCAGCAGAGTTCGAGAAAGCGAAGCCGAATTCG 1060
DB 1313 ATGCCAAGAACAGCTGGAGGCTGGAGGATGCCCTGCGAAGGCCCAAGCAGACCTGG 1372
QY 1061 CCCAGCATCAGAGAAATA 1079
DB 1373 CCCGGCTGCTGAAGGAGTA 1391

RESULT 8

US-10-393-567-61
; Sequence 61, Application US/10393567
; Publication No. US20030194733A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
; FILE REFERENCE: CDS 269 US NP
; CURRENT APPLICATION NUMBER: US/10/393,567
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,667
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: human
US-10-393-567-61

Query Match 3.1%; Score 37.4; DB 15; Length 2270;
Best Local Similarity 49.2%; Pred. No. 0.42;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 881 CTCAGGCCAGAACGAGATCTCTGAACCGCGTTATGAGCTGGCCAGAGCCGGTGATTT 940
DB 1193 CTGAGATCAACCGCATCCAGAGGCTGAGATCTGAGATCGACACGTCAGAGCAGT 1252
QY 941 GCGGCTACCACTGGCAGAGTGTGATGTCGCCGGGTAGTGGATCTGCCGTGTGG 1000
DB 1253 GCGCCAACTGCAGCGCGCCATTGCTGATCTGAGCAGCGTGGGAGAGTGCCCTCAAG 1312
QY 1001 CGACCTGTCATACCAACCGCGTTCCAGCAGAGTTCGAGAAAGCGAAGCCGAATTCG 1060
DB 1313 ATGCCAAGAACAGCTGGAGGCTGGAGGATGCCCTGCGAAGGCCCAAGCAGACCTGG 1372
QY 1061 CCCAGCATCAGAGAAATA 1079
DB 1373 CCCGGCTGCTGAAGGAGTA 1391

RESULT 9

US-10-394-087-61
; Sequence 61, Application US/10394087
; Publication No. US20030194734A1
; GENERAL INFORMATION:
; APPLICANT: Jatkoe, Tim
; TITLE OF INVENTION: SELECTION OF MARKERS
; FILE REFERENCE: CDS 265 US NP
; CURRENT APPLICATION NUMBER: US/10/394,087
; CURRENT FILING DATE: 2003-03-21

; PRIOR APPLICATION NUMBER: 60/368,790
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: human
US-10-394-087-61

Query Match 3.1%; Score 37.4; DB 15; Length 2270;
Best Local Similarity 49.2%; Pred. No. 0.42;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 881 CTCAGGCCAGAACGAGATCTCTGAACCGCGTTATGAGCTGGCCAGAGCCGGTGATTT 940
DB 1193 CTGAGATCAACCGCATCCAGAGGCTGAGATCTGAGATCGACACGTCAGAGCAGT 1252
QY 941 GCGGCTACCACTGGCAGAGTGTGATGTCGCCGGGTAGTGGATCTGCCGTGTGG 1000
DB 1253 GCGCCAACTGCAGCGCGCCATTGCTGATCTGAGCAGCGTGGGAGAGTGCCCTCAAG 1312
QY 1001 CGACCTGTCATACCAACCGCGTTCCAGCAGAGTTCGAGAAAGCGAAGCCGAATTCG 1060
DB 1313 ATGCCAAGAACAGCTGGAGGCTGGAGGATGCCCTGCGAAGGCCCAAGCAGACCTGG 1372
QY 1061 CCCAGCATCAGAGAAATA 1079
DB 1373 CCCGGCTGCTGAAGGAGTA 1391

RESULT 10

US-09-919-172-34
; Sequence 34, Application US/09919172
; Patent No. US20020119463A1
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 34
; LENGTH: 2310
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020119463A1 008513.49
; NAME/KEY: unsure
; LOCATION: 2307
; OTHER INFORMATION: a, t, c, g, or other
US-09-919-172-34

Query Match 3.1%; Score 37.4; DB 9; Length 2310;
Best Local Similarity 49.2%; Pred. No. 0.42;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 881 CTCAGGCCAGAACGAGATCTCTGAACCGCGTTATGAGCTGGCCAGAGCCGGTGATTT 940
DB 1203 CTGAGATCAACCGCATCCAGAGGCTGAGATCTGAGATCGACACGTCAGAGCAGT 1262
QY 941 GCGGCTACCACTGGCAGAGTGTGATGTCGCCGGGTAGTGGATCTGCCGTGTGG 1000
DB 1263 GCGCCAACTGCAGCGCGCCATTGCTGATCTGAGCAGCGTGGGAGAGTGCCCTCAAG 1322
QY 1001 CGACCTGTCATACCAACCGCGTTCCAGCAGAGTTCGAGAAAGCGAAGCCGAATTCG 1060
DB 1323 ATGCCAAGAACAGCTGGAGGCTGGAGGATGCCCTGCGAAGGCCCAAGCAGACCTGG 1382

```
QY 1061 CCCAGCATCAGAGAAATA 1079
      |||||
Db 1383 CCCGGCTGCTGAAGGAGTA 1401

RESULT 11
US-09-974-298-42
; Sequence 42, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Cheg, Hwei-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 42
; LENGTH: 2310
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 008513.49
; NAME/KEY: unsure
; LOCATION: 2307
; OTHER INFORMATION: a, t, c, g, or other
US-09-974-298-42

Query Match 3.1%; Score 37.4; DB 9; Length 2310;
Best Local Similarity 49.2%; Pred. No. 0.42;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 881 CTCAGCGCCAGAACGAGATCTCGAAACGGGTATGAGCTGGCGGAGTGGGATCTGCGGTGATT 940
      |||||
Db 1203 CTGAGATCAACCGCATGATCCAGAGGCTGAGATCTGAGATCGACCACTCAAGACGCT 1262
      |||||
QY 941 GCGGCTACCACTGGCAGAGTGTGATGCGCGGGGTAGTGGATCTGCGGTGTTGG 1000
      |||||
Db 1263 GCGCAACCTGCGAGCGGCCCATGCTGTGATGCTGAGCAGCGTGGGAGATGCCCTCAAGG 1322
      |||||
QY 1001 CGACCCCTGATACCAACCGCGGTTCCAGCAGAGTTGAGAAAGCGAAGCCGATTCG 1060
      |||||
Db 1323 ATGCCAAGAACCAAGCTGGGAAGGCTGGAGGATGCCCTGCAGAGGCGCAAGACGACCTGG 1382
      |||||
QY 1061 CCCAGCATCAGAGAAATA 1079
      |||||
Db 1383 CCCGGCTGCTGAAGGAGTA 1401

RESULT 13
US-10-027-632-279124/c
; Sequence 279124, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 279124
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Human
; OTHER INFORMATION:
US-10-027-632-279124

Query Match 3.0%; Score 37; DB 13; Length 639;
Best Local Similarity 58.7%; Pred. No. 0.26;
Matches 64; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 496 GGTCCATTGCGTTTCTCAACGATCAGCGGCTGATGAACAGGGGCGGCTGCTGCGCAAC 555
      |||||
Db 593 GGTGGAGTGGGAGTTTCTACATGAGGCGCTGCAGCTTCAGGGTTGGCTGCTGCCCTC 534
      |||||
QY 556 ACCGAACGCGGTAAGCTGCGGCGGAAGATGCAACCTGAGCAGTGGCG 604
      |||||
Db 533 CCCCAAGGAGCTCAGATGCTTAGACAGCAGGCGACAGCAGTGGTG 485
      |||||

; OTHER INFORMATION: Incyte ID No. 008513.49
; NAME/KEY: unsure
; LOCATION: 2307
; OTHER INFORMATION: a, t, c, g, or other
US-10-116-802-210

Query Match 3.1%; Score 37.4; DB 13; Length 2310;
Best Local Similarity 49.2%; Pred. No. 0.42;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 881 CTCAGCGCCAGAACGAGATCTCGAAACGGGTATGAGCTGGCGGAGTGGGATCTGCGGTGATT 940
      |||||
Db 1203 CTGAGATCAACCGCATGATCCAGAGGCTGAGATCTGAGATCGACCACTCAAGACGCT 1262
      |||||
QY 941 GCGGCTACCACTGGCAGAGTGTGATGCGCGGGGTAGTGGATCTGCGGTGTTGG 1000
      |||||
Db 1263 GCGCAACCTGCGAGCGGCCCATGCTGTGATGCTGAGCAGCGTGGGAGATGCCCTCAAGG 1322
      |||||
QY 1001 CGACCCCTGATACCAACCGCGGTTCCAGCAGAGTTGAGAAAGCGAAGCCGATTCG 1060
      |||||
Db 1323 ATGCCAAGAACCAAGCTGGGAAGGCTGGAGGATGCCCTGCAGAGGCGCAAGACGACCTGG 1382
      |||||
QY 1061 CCCAGCATCAGAGAAATA 1079
      |||||
Db 1383 CCCGGCTGCTGAAGGAGTA 1401

RESULT 12
US-10-116-802-210
; Sequence 210, Application US/10116802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 210
; LENGTH: 2310
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 18:46:46 ; Search time 2464 Seconds
(Without alignments)
14846.255 Million cell updates/sec

Title: US-09-807-990-1
Perfect score: 1225
Sequence: 1 ctgcaggcgaaagcaatgt.....taagatcatgtgcggttaac 1225

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513283 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estoc.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_iod.*
26: em_gss_pbg.*
27: em_gss_vil.*
28: gb_ges1.*
29: gb_ges2.*

Result No.	Score	Match	Length	DB	ID	Description
C 1	60.2	4.9	827	28	BZ571331	BZ571331: msh2_1837
C 2	51.4	4.2	793	28	BZ571419	BZ571419 msh2_1877
C 3	41.6	3.4	1002	28	BZ566646	BZ566646 pace2-164
4	41	3.3	1201	13	BX381961	BX381961 BX381961

Result No.	Score	Match	Length	DB	ID	Description
C 1	60.2	4.9	827	28	BZ571331	BZ571331: msh2_1837
C 2	51.4	4.2	793	28	BZ571419	BZ571419 msh2_1877
C 3	41.6	3.4	1002	28	BZ566646	BZ566646 pace2-164
4	41	3.3	1201	13	BX381961	BX381961 BX381961

Result No.	Score	Match	Length	DB	ID	Description
C 1	60.2	4.9	827	28	BZ571331	BZ571331: msh2_1837
C 2	51.4	4.2	793	28	BZ571419	BZ571419 msh2_1877
C 3	41.6	3.4	1002	28	BZ566646	BZ566646 pace2-164
4	41	3.3	1201	13	BX381961	BX381961 BX381961

Result No.	Score	Match	Length	DB	ID	Description
C 1	60.2	4.9	827	28	BZ571331	BZ571331: msh2_1837
C 2	51.4	4.2	793	28	BZ571419	BZ571419 msh2_1877
C 3	41.6	3.4	1002	28	BZ566646	BZ566646 pace2-164
4	41	3.3	1201	13	BX381961	BX381961 BX381961

Result No.	Score	Match	Length	DB	ID	Description
C 1	60.2	4.9	827	28	BZ571331	BZ571331: msh2_1837
C 2	51.4	4.2	793	28	BZ571419	BZ571419 msh2_1877
C 3	41.6	3.4	1002	28	BZ566646	BZ566646 pace2-164
4	41	3.3	1201	13	BX381961	BX381961 BX381961

source	1. .827	/organism="Pseudomonas aeruginosa"	
		/mol_type="genomic DNA"	
		/strain="WSH"	
		/db_xref="taxon:287"	
		/clone="msh2_1817"	
		/notes="Environmental isolate. Whole genomic shotgun library."	
ORIGIN			
Query Match	4.9%;	Score 60.2;	DB 28; Length 827;
Best Local Similarity	55.5%;	Pred. No. 1.6e-05;	
Matches	116;	Conservative	0; Mismatches 93; Indels 0; Gaps 0;
QY	817	TCCTATCCGTCGGGCAATACCTCTATCGGTGGGCTACTCGCGTGGTGGTGGCAGAGATC	876
DB	376	TCCTATCCGTCGGGCAATACCTCTATCGGTGGGCTACTCGCGTGGTGGTGGCAGAGATC	317
QY	877	AACCTCAGCGCCAGAACAGATCCTGAAACGGGTTATGAGCTGGGCCAGAGCCGGGTG	936
DB	317	GTCCCGGAGATCAGATCGATGGTCTTCGCCCGCCGCGAGAGATCGGAGAGCCGGTGTG	258
QY	937	ATTGCGGCTACCATCGGAGAGTGTGATGTCGCCCGCGGGTAGTGGGATCTGCCGTT	996
DB	257	CTGGCCGGGTGACCTTCGCCAGCCTTGGAAAGCGCGGAGACCGCGCGCGCGGTG	198
QY	997	GTGGCGGACC	1005
DB	197	GTGGCGGAGC	189
RESULT 3			
LOCUS	BZ566646	1002 bp	DNA linear GSS 17-DEC-2002
DEFINITION	pac82-164_5502.y2 pac82-164 Pseudomonas aeruginosa genomic clone		
ACCESSION	BZ566646		
VERSION	BZ566646.1	GI:27196581	
KEYWORDS	GSS.		
SOURCE	Pseudomonas aeruginosa		
ORGANISM	Pseudomonas aeruginosa		
REFERENCE	1 (bases 1 to 1002)		
AUTHORS	Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.		
TITLE	Whole-Genome-Sequence variation among multiple isolates of Pseudomonas aeruginosa library		
JOURNAL	J. Bacteriol. (2002) In press		
COMMENT	Contact: Chris K. Raymond Genome Center University of Washington Box 352145, Seattle, WA 98105-2145, USA Tel: 2062216954 Fax: 2066857244 Email: craymond@u.washington.edu Class: shotgun.		
FEATURES	Location/Qualifiers		
source	1. .1002	/organism="Pseudomonas aeruginosa"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:287"	
		/clone="pac82-164_5502"	
		/clone_lib="pac82-164"	
		/notes="clinical isolate 2-164 Whole genomic shotgun library."	
ORIGIN			
Query Match	3.4%;	Score 41.6;	DB 28; Length 1002;
Best Local Similarity	54.6%;	Pred. No. 3.5;	
Matches	83;	Conservative	0; Mismatches 69; Indels 0; Gaps 0;
QY	817	TCCTATCCGTCGGGCAATACCTCTATCGGTGGGCTACTCGCGTGGTGGTGGCAGAGATC	876
DB	391	TCCTATCCGTCGGGCAATACCTCTATCGGTGGGCTACTCGCGTGGTGGTGGCAGAGATC	450
QY	877	AACCTCAGCGCCAGAACAGATCCTGAAACGGGTTATGAGCTGGGCCAGAGCCGGGTG	936
DB	451	GTCCCGGAGATCAGATCGATGGTCTTCGCCCGCGCGAGAGATCGGAGAGCCGGGTG	510
QY	937	ATTGCGGCTACCATCGGAGAGTGTGATGTCGCCCGCGGGTAGTGGGATCTGCCGTT	968
DB	511	CTGGCGGCGTGCACCTTTCCCGAGCAGCTTGA	542

[illegible]


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Db      947 SSSSAVSSGCGVSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 1006
QY      476 TGCOCACACCGCGGCTGCGCTCATTGCTTCTAACGATCAGCGCATGATGAAC 535
Db      1007 SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 1066
QY      536 AGGGGCGCTGCTGCGCAACCGGAGCGGTAAGCTGCGCGGAGAGTGCACACTGA 595
Db      1067 AASGGAASAGVSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 1126
QY      596 GCGATGCGCGGCTGCGCAATGCTTCTCGCGCGCGTTCGTAGCCGATCACGAAAAAG 655
Db      1127 SSSAASRSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 1186
QY      656 ACGCCCGCGCGCTGC 670
Db      1187 AMAASSSSSSSSSSSV 1201

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RESULT 8
LOCUS   CF267657 577 bp mRNA linear EST 13-AUG-2003
DEFINITION TgSTzy198f07.y1 TgMAS Tachyzoite cDNA Library Toxoplasma gondii
ACCESSION CF267657
VERSION   CF267657.1 GI:33629610
KEYWORDS EST.
SOURCE   Toxoplasma gondii
ORGANISM Toxoplasma gondii
REFERENCE 1 (bases 1 to 577)
AUTHORS Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioke,J.A., White,M.,
Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,
Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I.,
Kennedy,S., Vagstad,L., Waterston,R. and Wilson,R.
TITLE Toxoplasma EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Clifton, S.
Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: toxowatson.wustl.edu
Contact David Sibley (toxowest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40RP from Gibco.

```

```

FEATURES
source
1. 577
/organism="Toxoplasma gondii"
/mol_type="mRNA"
/strain="Tachyzoite"
/db_xref="taxon:5811"
/clone="TgSTzy198f07.y1"
/dev_stage="Tachyzoite"
/lab_host="ElectroTen Blue cells (Stratagene)"
/clone_lib="TgMAS Tachyzoite cDNA library"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed by Keliang Tang,
and Robert Cole at Washington University. cDNA was
synthesized from Poly(A)+ mRNA using an oligo-d(T) primer
containing a XhoI site. Following second strand synthesis,
EcoRI adapters were ligated to the cDNA, and products were
size-selected on sephacryl S500. The cDNA were
directionally cloned into the EcoRI/XhoI prepared
pBluescript II SK+ vector, and electroporated into
ElectroTen Blue cells (Stratagene). The library may
contain a small percentage of host or bacterial
contaminants."

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ORIGIN

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Query Match 3.3%; Score 40; DB 14; Length 577;
Best Local Similarity 49.5%; Pred. No. 7.8;
Matches 103; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 589 AACCTGACGAGTGGCGGGTGGCGAATGCTTTCTCGGCGCGCTTTGGTAGCCCGATCACC 648
Db 206 AGATGACTGTTTCAGCGGTAGGAAAGTGTTCATCGCGGGATTTCATGTCACCCACAAA 265
QY 649 GAAAGAGACCCCGCGCTGCATAATTAATTAACCAATATGATTAAGGAGCGCGGGAT 708
Db 266 AGAAGCAACACCCCTCCAGTGTCCCAAGTTCCTTCGATGATGCGCAGAGAACTGTGAGGT 325
QY 709 CTGGCCACCCGCGAGCGGAAAGATCACTATCGGATTCGTCGTTTCGGTTCGGTTTATGGG 768
Db 326 GAAGGAACCTGTAGTTTGGACGATTCGATCGTCTTGTTCGGCGGACTTCAATGCT 385
QY 769 GTCTCTACCTGTAATACCAACCGAGCAGG 796
Db 386 CGGTTGACATGAAGACATCCGAGGAGG 413

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RESULT 9
LOCUS   BZ578090 940 bp DNA linear GSS 17-DEC-2002
DEFINITION msh2_5712.x1 msh Pseudomonas aeruginosa genomic clone msh2_5712,
genomic survey sequence.
ACCESSION BZ578090
VERSION   BZ578090.1 GI:27213151
KEYWORDS GSS.
SOURCE   Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
REFERENCE 1 (bases 1 to 940)
AUTHORS Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
TITLE Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
JOURNAL J. Bacteriol. (2002) In press
COMMENT Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

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FEATURES
source
1. 940
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="M5H"
/db_xref="taxon:287"
/clone="msh2_5712"
/clone_lib="msh"
/notes="Environmental isolate. Whole genomic shotgun
library."

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ORIGIN
Query Match 3.2%; Score 39.8; DB 28; Length 940;
Best Local Similarity 51.1%; Pred. No. 11;
Matches 92; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 538 GGGCGCTGCTCGGCAACACCGACCGGTAGCTGGCGCGGAGATGATCAACCTGAGC 597
Db 595 GCGACCCAGTTGAGCAGCGCGCGCTTCGGCAACACACAGATGCTGGTGGCGCGCGC 654
QY 598 AGTGCGCGGGTGGCAATGCTTCTCCGCGCGGTTGGTAGCCCGATCACCGAAAAGAC 657
Db 655 ACCGCGCAACTGAACGCTTCTCACCCTCCCGTGGGTTGCGAGTGACCGGTCAATGCC 714
QY 658 GCCCGCGCGCTGCATTAATTAATGACCAATATGATTGAGAGCGCGCGGATCTGCGGACC 717

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RESULT 12
BX425011/c
LOCUS
DEFINITION
BX425011 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOB0A007ZB02
3-PRIME, mRNA sequence.
ACCESSION
BX425011
VERSION
BX42501.1 GI:30774426
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 907)
Li W.B., Gruber C., Jessee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1077.f for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOB0A007ZB02P1&cluster=1077.f. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOB0A007ZB02P1.
Location/Qualifiers
1..907
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CLOB0A007ZB02"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
ORIGIN
Query Match 3.2%; Score 39.2; DB 13; Length 907;
Best Local Similarity 43.5%; Pred. No. 16;
Matches 93; Conservative 16; Mismatches 105; Indels 0; Gaps 0;
QY 126 GGGTTCCCGGCGCGCTTTTATGAGGCGGCGGAGGCGGTATCTGTCGCCCT 185
DB 350 KGGTYCCCGCCCTCTCTTTTATGAGGCGGCGGAGGCGGTATCTGTCGCCCT 291
QY 186 GTTTCGCGACAGCGTTTATGTAATTTTGTGACGTATATCAGTTTAAAGCA 245
DB 290 TTTTTCACCCCTTTTATGTAATTTTGTGACGTATATCAGTTTAAAGCA 231
QY 246 CCTGTGGCGCTCATCTCGCAACCTGTTGATTAAGCAACACTCTTCACTCAGCAAT 305
DB 230 CCCCCCCCCCTTTTTCACCAACCAATAATWTKGGGKKTTTDDRAAAAAAAA 171
QY 306 TAACAGCAGCAGTAAGGTATACGATGAAAAA 339
DB 170 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 137
RESULT 13
BQ815676
LOCUS
DEFINITION
BQ815676 704 bp mRNA linear EST 01-AUG-2002
103052B06.x1 C. reinhardtii CC-1690, Deflagellation (normalized),
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION
BQ815676
VERSION
BQ815676.1 GI:22064197
KEYWORDS
EST.
SOURCE
Chlamydomonas reinhardtii

ORGANISM
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE
1 (bases 1 to 704)
Grosman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C.,
Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1030
Unpublished (2002)
JOURNAL
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
Location/Qualifiers
1..704
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Deflagellation
(normalized), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
XhoI; Deflagellation library, constructed by John Davies
and Jeffrey McDermott, combines cDNAs from CC-1690 cells
which had been re-synthesizing flagella for 15, 30 and 60
min after being deflagellated by pH shock. PolyA mRNA was
purified from each sample, pooled and cDNA synthesized.
The cDNA was directionally cloned into lambda Zap II
(Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al., (1996) Genome Research 6: 791-806."
ORIGIN
Query Match 3.1%; Score 38.2; DB 13; Length 704;
Best Local Similarity 45.9%; Pred. No. 28;
Matches 130; Conservative 0; Mismatches 153; Indels 0; Gaps 0;
QY 377 CTCAGCCCTCGGCGTGTGCTACCGGCAACGACACTACCAACCGGATCTCTACT 436
DB 43 CTGAGGTGTGAGCTGTGGCGGCAACGCGCGCGACACAAAGAACCGCATCGTTC 102
QY 437 ACTCAAGAACAGTGAAGCCATTAAACAGCTGGCGCTGTTCGCCACACCGCGGTGG 496
DB 103 CCGGCCACATTACGTGGGCCATTTCGCAACGACGAGGAGCTGGGCAAGCTGCTGGCGAGG 162
QY 497 GCTCCATTCGGTTTCTCAACGATCAGGCCATGATGACAGGGGGCGCTCTCGGCAACA 556
DB 163 TGACCATTCATCGGCGGCTGTGCTGCCCAACATCCAGCGCGTGTCTGCCAAGAGA 222
QY 557 CCGAACCGCGTAACTGGCGGCGGAGAGATGCAAACTGACAGCTGGCGGCGTGGCGATG 616
DB 223 CCAAGCGCGCAAGCGCGGAGGACGGCTCGCGCGCGCTGTAAACGGGCTGCTGGCGGTG 282
QY 617 CTTTCTCCGCGCGTGTGGTAGCCCGCATCACGAAAAAGACGC 659
DB 283 GCGGGGCTTCCCGCGCAGCTACCTCCATCTTCTTCAATCCCC 325
RESULT 14
BX446497
LOCUS
DEFINITION
BX446497 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOB0A009ZE10
5-PRIME, mRNA sequence.
ACCESSION
BX446497
VERSION
BX446497.1 GI:31033734
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8860.f
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOB009ZE10RP1.
FEATURES
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/organism="Homo sapiens"
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/clone="CLOB009ZE10"
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/clone_lib="Homo sapiens PLACENTA"
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with a NotI-o-igo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pcwvSPORT 6 vector.
Library was not normalized."
ORIGIN
Query Match 3.1%; Score 38.2; DB 13; Length 1201;
Best Local Similarity 40.7%; Pred. No. 35;
Matches 46; Conservative 25; Mismatches 42; Indels 0; Gaps 0;
Qy 110 TACTGAGCGCGCGGGGGTCCCGGCGCGCTTTTATGGGCTGCGGTGAGGAC 169
Db 957 TBCCGCGGGGGCGCGCTTMCSSKYCCGCTTTTCTAGKGBCCCTTTNNRNK 1016
Qy 170 GTTATCTCGCGCTGTTCTGCAACAACGCTTTTATGTGTAATTTTGT 222
Db 1017 GNNRNVS CGGSBGBBKXKBKXGSSSTTTTTTTT TTTTTTTT 1069

RESULT 15
CC735352 698 bp DNA linear GSS 23-JUN-2003
LOCUS OG0UB85IV_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMMBMA0452P02,
DEFINITION genomic survey sequence.
ACCESSION CC735352
VERSION CC735352.1 GI:32158289
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 698)
AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, J.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other GSSs: OG0UB85TH
Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
location/Qualifiers

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1..698
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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Best Local Similarity 48.6%; Pred. No. 32;
Matches 104; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
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Db 89 CCRGAAGACGATCCTGCTGGCGCGCGCTCGAGCTCCCGCGCGCGGGCGGTCCC 148
Qy 573 GCGCGCGGAGATGCAACCTGAGCAGTGGGGGGTGGCGAATGCTTTTCGGGCGGTT 632
Db 149 CGACCGGACGGTGAAGTGTGTCGTAGACGGGTAGCGGCAGTCGTCGGCGGGGAGGC 208
Qy 633 TGGTAGCCCGATCACCGAAAGAGCGCCCGCGCTGCATATAATTACTGACCAATATGAT 692
Db 209 TGGCGGCGAGGTGCGCGAAGCGCGCGCGCGCGCGCGCTTCTCCACCCACCGCGCT 268
Qy 693 TGAGGACCGCGGGATCTGGCGGACCGCGCGCGG 726
Db 269 CGAGCGGCTGCTCGACCTTGACACCCACGAGAGCG 302

Search completed: June 4, 2004, 20:40:31
Job time : 2469 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 18:49:36 ; Search time 85 Seconds
(without alignments)
7997.822 Million cell updates/sec

Title: US-09-807-990-1

Perfect score: 1225

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	750	61.2	750	3	US-09-417-090-6
4	750	61.2	750	4	US-09-727-578-6
5	514.6	42.0	762	4	US-09-489-039A-762
6	507	41.4	747	3	US-08-750-145A-19
7	507	41.4	747	3	US-08-975-698A-23
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9	507	41.4	747	3	US-09-727-578-23
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11	493.4	40.3	747	3	US-08-975-698A-25
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13	493.4	40.3	747	3	US-09-727-578-25
14	422	34.4	747	3	US-08-750-145A-2
15	422	34.4	750	3	US-08-975-698A-2
16	422	34.4	750	3	US-09-417-090-2
17	422	34.4	750	3	US-09-727-578-2
18	357.4	29.2	747	3	US-08-750-145A-17
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28	60.2	4.9	762	4	US-09-252-991A-11386	Sequence 11986, A
29	60.2	4.9	1125	4	US-09-252-991A-11956	Sequence 11956, A
30	44.6	3.6	2832	4	US-09-540-236-1538	Sequence 1538, Ap
31	44.6	3.6	62909	4	US-09-596-302-32	Sequence 32, Appl
32	37.4	3.1	2310	4	US-09-919-172-34	Sequence 34, Appl
33	37.2	3.0	1974	4	US-09-489-039A-3050	Sequence 3050, Ap
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ALIGNMENTS

RESULT 1
US-08-750-145A-9
: Sequence 9, Application US/08750145A
: Patent No. 6010851
: GENERAL INFORMATION:
: APPLICANT: MIHARA, Yasuhiro
: APPLICANT: UTAGAWA, Takashi
: APPLICANT: YAMADA, Hideaki
: APPLICANT: ASANO, Yasuhisa
: TITLE OF INVENTION: Method for Producing Nucleoside-5'-
: TITLE OF INVENTION: Phosphate Ester
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
: STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
: CITY: ARLINGTON
: STATE: VA
: COUNTRY: USA
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/750,145A
: FILING DATE: 01-JAN-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 7-149781
: FILING DATE: 05-May-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 8-094680
: FILING DATE: 26-Mar-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: NORMAN F. OBLON
: REGISTRATION NUMBER: 24,618
: REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-413-3000
: TELEFAX: 703-413-2220
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 750 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO

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; ORIGINAL SOURCE:
; ORGANISM: Escherichia blattae
; STRAIN: JCM 1650
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..747
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US-08-750-145A-9

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Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-08-975-698A-6
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; Sequence 6, Application US/08975698A
; Patent No. 6015697
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIRO
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; TITLE OF INVENTION: ESTER
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,698A
; FILING DATE: 21-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0855-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 750 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
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; ORGANISM: Escherichia blattae
; STRAIN: JCM 1650
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Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1051 GCCGAAATTCGCCAGCATCAGAGAAATAA 1080
Db 721 GCCGAAATTCGCCAGCATCAGAGAAATAA 750

RESULT 3
US-09-417-090-6
Sequence 6, Application US/09417090
Patent No. 6207435
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
UTAGAWA, TAKASHI
YAMADA, HIDEAKI
ASANO, YASUHIRO
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,090
FILING DATE: 13-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE: 21-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 750 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia blattae
STRAIN: JCM 1650
FEATURE:
NAME/KEY: CDS
LOCATION: 1..747
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NAME/KEY: sig_peptide
LOCATION: 1..54
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US-09-417-090-6
Query Match 61.2%; Score 750; DB 3; Length 750;
Best Local Similarity 100.0%; Pred. No. 1.2e-239; Mismatches 0; Indels 0; Gaps 0;
Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 331 ATGAAAAACGTTCTGCGAGTTTGTTCGCGATTGTTTTCGCGATTGTTTCTCTCTCAGGCGCTGGG 390
Db 1 ATGAAAAACGTTCTGCGAGTTTGTTCGCGATTGTTTTCGCGATTGTTTCTCTCTCAGGCGCTGGG 60
QY 391 CTGTCGCTACCGCAACGACACTACGAGAAACCGGATCTCTACTCTCAAGACAGT 450
Db 61 CTGTCGCTACCGCAACGACACTACGAGAAACCGGATCTCTACTCTCAAGACAGT 120
QY 451 GAAGCCATTACAGCTGCGGCTGTGCGCCACACCGCGCTGGCTCCATTGGCTTT 510
Db 121 GAAGCCATTACAGCTGCGGCTGTGCGCCACACCGCGCTGGCTCCATTGGCTTT 180
QY 511 CTCACGATCAGGCGCATGTATGAACAGGCGCGCTGCTGCGCAACACCGAAGCGGTAAAG 570
Db 181 CTCACGATCAGGCGCATGTATGAACAGGCGCGCTGCTGCGCAACACCGAAGCGGTAAAG 240
QY 571 CTGGCGCGGAAGATGCAAACTGAGCAGTGGCGGGTGGCGAATGCTTTCTCGGGCGG 630
Db 241 CTGGCGCGGAAGATGCAAACTGAGCAGTGGCGGGTGGCGAATGCTTTCTCGGGCGG 300
QY 631 TTTGGTAGCCGATCAGGAAAGAGCGCCCGCGCTGCATTAATTAATTAATTAATG 690
Db 301 TTTGGTAGCCGATCAGGAAAGAGCGCCCGCGCTGCATTAATTAATTAATTAATG 360
QY 691 ATTGAGGACCGCGGGATCTGCGGACCGCGAGCGGAAAGATCACTATATGCGCATTCGT 750
Db 361 ATTGAGGACCGCGGGATCTGCGGACCGCGAGCGGAAAGATCACTATATGCGCATTCGT 420
QY 751 CCGTTCGGTTTATGGGCTCTACCTGTAATACACCGAGCAGGACAACTGTCGAAA 810
Db 421 CCGTTCGGTTTATGGGCTCTACCTGTAATACACCGAGCAGGACAACTGTCGAAA 480
QY 811 AATGGCTCTTATCGGCTGCTACCTGTAATACACCGAGCAGGACAACTGTCGAAA 870
Db 481 AATGGCTCTTATCGGCTGCTACCTGTAATACACCGAGCAGGACAACTGTCGAAA 540
QY 871 GAGATCAACCTCAGCGCCAGAACGAGATCCTGAAACCGGTTATGAGCTGGGCCAGAGC 930
Db 541 GAGATCAACCTCAGCGCCAGAACGAGATCCTGAAACCGGTTATGAGCTGGGCCAGAGC 600

QY 931 CGGGTGAATTTGGCGCTACCACTGGCAGAGTATGGATGATCCGGCGGGTAGTGGGATCT 390
Db 601 CGGGTGAATTTGGCGCTACCACTGGCAGAGTATGGATGATCCGGCGGGTAGTGGGATCT 660
QY 991 GCGGTGTGGCGACCCCTGCTATACCAACCCGGCGGTTCAGCAGCAGTTCAGAAAGCGAAG 1050
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Db 721 GCCGAATTCGCCAGCATCAGAGAAATAA 750

RESULT 4
US-09-727-578-6
; Sequence 6, Application US/09727578
; Patent No. 6355472
; GENERAL INFORMATION:
; APPLICANT: MIHARA, YASUHIRO
; APPLICANT: UTAGAWA, TAKASHI
; APPLICANT: YAMADA, HIDEAKI
; APPLICANT: ASANO, YASUHIRO
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
; TITLE OF INVENTION: ESTER
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/727,578
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,698
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0010-0885-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 750 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYDROTHERMAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia blattae
; STRAIN: JCM 1650
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..747
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; NAME/KEY: sig_peptide
; LOCATION: 1..54
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 55..747
; US-09-727-578-6

Query Match 61.2%; Score 750; DB 4; Length 750;
Best Local Similarity 100.0%; Pred. No. 1.2e-239;
Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 331 ATGAAAAACGTGTCTTGGCAGTTTGTTCGCCGATGTCTCTTCTCAGGCCCTCGCG 390
Db 1 ATGAAAAACGTGTCTTGGCAGTTTGTTCGCCGATGTCTCTTCTCAGGCCCTCGCG 60
QY 391 CTGGTCGCTACCGGCAACGACACTACACGAAACCGGATCTCTACTACTCTCAAGAACAGT 450
Db 61 CTGGTCGCTACCGGCAACGACACTACACGAAACCGGATCTCTACTACTCTCAAGAACAGT 120
QY 451 GAAGCCATTAAACAGCTGGCGCTGTTCGCCGACACCCGCGGTGGGTCTCATTCGCTTT 510
Db 121 GAAGCCATTAAACAGCTGGCGCTGTTCGCCGACACCCGCGGTGGGTCTCATTCGCTTT 180
QY 511 CTCAAACGATCAGGCCATGTATGAACAGGGGCGCTGTGCGCAACACCGAACGCGGTAA 570
Db 181 CTCAAACGATCAGGCCATGTATGAACAGGGGCGCTGTGCGCAACACCGAACGCGGTAA 240
QY 571 CTGGCGCGGAAGATGCAACCTGAGCAGTGTGGCGGGTGGGGAATGCTTTCTCGCGCGG 630
Db 241 CTGGCGCGGAAGATGCAACCTGAGCAGTGTGGCGGGTGGGGAATGCTTTCTCGCGCGG 300
QY 631 TTTGGTAGCCCGATCACCGAAAAAGACGCCCGCGGTGGCATTAATTAATTAATTAATG 690
Db 301 TTTGGTAGCCCGATCACCGAAAAAGACGCCCGCGGTGGCATTAATTAATTAATTAATG 360
QY 691 ATTGAGGACGCGGGGATCTGGCGACCGCGAGCGGGAAGATCACTATATGGCATTCGT 750
Db 361 ATTGAGGACGCGGGGATCTGGCGACCGCGAGCGGGAAGATCACTATATGGCATTCGT 420
QY 751 CCGTTTCGGGTTTATGGGTTCTTACCTGTATATACACCGAGCAGCAAACTGTCCAAA 810
Db 421 CCGTTTCGGGTTTATGGGTTCTTACCTGTATATACACCGAGCAGCAAACTGTCCAAA 480
QY 811 AATGGCTCTTATCCGTCGGCGATACCTCTATCGCTGGCTACTCGCTGGCTGGTGGCA 870
Db 481 AATGGCTCTTATCCGTCGGCGATACCTCTATCGCTGGCTACTCGCTGGCTGGTGGCA 540
QY 871 GAGATCAACCTCAGCGCCAGAACGAGATCTGAAACCGGTTATGAGCTGGGCCAGAGC 930
Db 541 GAGATCAACCTCAGCGCCAGAACGAGATCTGAAACCGGTTATGAGCTGGGCCAGAGC 600
QY 931 CCGGTGATTTCGGCTACCACTGGCAGATGATGATGCGCGGGGTATGGATCT 990
Db 601 CCGGTGATTTCGGCTACCACTGGCAGATGATGATGCGCGGGGTATGGATCT 660
QY 991 GCGGTGTGGGACCCCTGCATACCAACCGCGGTTCAGCAGCAGTTCAGAAAGCGAAG 1050
Db 661 GCGGTGTGGGACCCCTGCATACCAACCGCGGTTCAGCAGCAGTTCAGAAAGCGAAG 720
QY 1051 GCCGAATTCGCCAGCATCAGAGAAATAA 1080
Db 721 GCCGAATTCGCCAGCATCAGAGAAATAA 750
RESULT 5
US-09-489-039A-762
; Sequence 762, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2799-2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 762

UTAGAWA, TAKASHI
YAMADA, HIDEAKI
ASANO, YASUHIKA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,090
FILING DATE: 13-Oct-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE: 21-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 1201C
FEATURE:
NAME/KEY: CDS
LOCATION: 1..744
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-417-090-23
Query Match 41.4%; Score 507; DB 3; Length 747;
Best Local Similarity 79.9%; Pred. No. 1.3e-158;
Matches 597; Conservative 0; Mismatches 150; Indels 0; Gaps 0;
QY 331 ATGAAAAACGGTTCTGGCAGTTGTTTGGCGCATTTCTTCTTCAGGCCCTGGG 390
DB 1 ATGAAAAACGGTTCTGGCCTCTGCTCGCCAGCGCTGTTTCGGTTAAOCCTTGGG 60
QY 391 CTGGTTCGCTACCGGCAACGACACTACGAAACCGGATCTCTACTACTCAGAACAGT 450
DB 61 CTGGTCCCTCGCGCAATGATCAACCAACCGGATCTCTATTATCTGAAAAATGCA 120
QY 451 GAAGCATTACAGCTGGCGCTGTGGCGCACCAACCGCGGTGGCTCCATTGGTTT 510
DB 121 CAGGCCATCGATGTCGCGCTGTGGCGCGCGCGGAGTTGGCAGCATCGCATTT 180
QY 511 CTCACGATCAGCCATGTATCAACAGGGCGCGCTCTCGCAACACCGAGCGGTAAG 570
DB 181 TTAACGATCAGCGCATGTATGAGAAAGACCGCTGTGGCAATACCGACGTGCAAG 240
QY 571 CTGGCGGGGAGAGTCAAACTGAGCAGTGGCGGGGTGGGAAATGCTTTCTCCGCGGG 630
DB 241 CTGGCGGCTGAAGATGCTAACTGAGCGCGCGGGGTGGCGAAATGCTTTCTCCAGCGCT 300

QY 631 TTTCGTAGCCCGATCACCGAAAAAGAGCCCGCGCTGCATAATTAATGACCAATATG 690
DB 301 TTTCGTAGCCCGATCACCGAAAAAGAGCCCGCGCTGCATAATTAATGACCAATATG 360
QY 691 ATTGAGGACCGCGGGATCTGGCGACCGCGAGCGGGAAGATCACTATATGCGATTGCT 750
DB 361 ATTGAGGATCGCGCGATCTGGCCACCGCGAGCGGGAAGAAATATATGCGATTGCT 420
QY 751 CGGTTGCGTTTATGGGCTCTCTACCTGTGAATACACCGAGCAGGACAAACTGTCCAAA 810
DB 421 CCGTTTGGGTTCTACGCGGTTTCACTGTGAATACCTACCGAGCAGGACAGTGTGGA 480
QY 811 AATGGCTCTATCGGTCCGGGCATACCTCTATGGCTGGGCTACTGCGCTGTGTGGCA 870
DB 481 AACGGATCTTACCTTTCGGCCATACCTCTATCGGTGGGCAACCGCGCTGCTACTGGG 540
QY 871 GAGATCAACCTTCAGCGCCAGAACGAGATCTGAAACGGGTTATGAGCTGGGCCAGAGC 930
DB 541 GAGATCAATCGCGAGCGCAAAACGAAATCTCAAACGGGCTATGAATGGGCGGAAAGC 600
QY 931 CGGGTGATTTGCGGCTACCACTGGCAGAGTGTATGGATGCCCGCGCGGTAGTGGGATCT 990
DB 601 CGGGTTATCTGCGGCTATCATTTGGCAGAGCATGTGATGCGCGCGGATGTGCGCTCG 660
QY 991 GCCGTTGTGGGACCTTCATACCAACCGCGGTTTCAGCAGCATGTCAGAAAGCGAAG 1050
DB 661 CGGGTGTGGGACCTTCATACCAACCGCGGTTTCAGCAGCATGTCAGAAAGCGAAG 720
QY 1051 GCGGAATTCGCCAGCATCAGAGAA 1077
DB 721 GATGAATTCGCCAAACCGCAGAGTAA 747

RESULT 9

US-09-727-578-23
Sequence 23, Application US/09727578
Patent No. 6355472
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIKA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
TITLE OF INVENTION: ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:
LENGTH: 747 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterobacter aerogenes
STRAIN: IFO 12010
FEATURE:
NAME/KEY: CDS
LOCATION: 1..744
US-09-727-578-23

Query Match 41.4%; Score 507; DB 4; Length 747;
Best Local Similarity 79.9%; Pred. No. 1.3e-158;
Matches 597; Conservative 0; Mismatches 150; Indels 0; Gaps 0;
QY 331 ATGAAAAAGCGTCTGGCAGTTGTTTGGCGCATGTTCTCTCAGGCCCTGGCG 390
DB 1 ATGAAAAAGCGGTTCTGCGCCTCTGCTCGCAGCGCTGTTTCGGTTAAGCTTCGG 60
QY 391 CTGCTGCTACCGGCAACGACACTTACCACGAAACCGGATCTCTACTACCTCAAGAACAGT 450
DB 61 CTGCTGCTCGCGGCANTGATGCAACCAACACCGGATCTCTATCTATCTGAAAAATGCA 120
QY 451 GAAGCCATTAAACAGCTTGGCGCTGTTTCGCGCCACCAACCGGGTGGGCTCATGCGTTT 510
DB 121 CAGGCCATCATAGTCTGGCGCTGTTTCGCGCGCGCGCGGAGTTGGCAGCATCGCATTT 180
QY 511 CTCAACGATCAGCCGATGATGACAGGCGGCTGCTGGCAACCGACCGGCGGTAAAG 570
DB 181 TTAACACATCAGGCGATGATGAAAGAGGCGGCTGTTGGCCAAATCGAACGTTGGCAAG 240
QY 571 CTGCGCGCGAAGATGAAACCTCAGCACTGGCGGGTGGCGAATGCTTTTCGCGGCGG 630
DB 241 CTGCGCGCTGAGATGCTAACTGAGCGCGCGCGCGGCGGATGCGCTTCTCCAGCGCT 300
QY 631 TTGTTAGCCCGATCAGCGAAAAAGAGCCCGCGGCTGCGAATTAATCTACCATATG 690
DB 301 TTGTTGTTGCCCATCAGCGAAAAAGAGCGCGCGGATGACATAAGCTGCTGACAAATATG 360
QY 691 ATTGAGACGCGGGATCTGGCAACCGCGAGCGGAGATCTATATGCGATTGCT 750
DB 361 ATTGAGATGCGCGGATCTGGCCACCGCGCGGAGGAGAAATATGCGCATTCGC 420
QY 751 CCGTTGCGGTTTATGGGGTCTCTACCTGTATATACCAACCGAGCAGCAAACTGTCCAAA 810
DB 421 CCGTTGCGGTTCTAGCGGTTTCAACCTGTAACTACCTAGCGAGCAGCAAGCTGTGAAA 480
QY 811 AATGCTCTTATCGTTCGGGATCTCTATCGCTGGGCTACGCGCTGCTGGTGCGCA 870
DB 481 AACGGATCTTACCTTCCGGCATACCTCTATGCTTGGGCAACCGCGCTGTACTGGCG 540
QY 871 GAGATCAACCTCAGCGCGCAGAACAGATCTCTGAAACGGGTATGAGCTGGCGCAGAGC 930
DB 541 GAGATCAATCGCAGCGCGAAACAGAAATCTCAACCGCGGTATGAATTGGCGGAAGC 600
QY 931 CGGTTGATTTGGCTACACTGGCAGAGTATGATGATGCGCGGGGTAGTGGATCT 990
DB 601 CGGTTATCTCGGCTATCATTTGGCAGAGCGATGTCGATCGCGCGGATGATGCTGCGCTG 660
QY 991 GCGTTTGGCGACCTGATACCAACCGCGGTTCCAGCAGCATGTCAGAAAGCGAG 1050
DB 661 GCGTTGGTGGACCTGATACCAACCGCGGTTCCAGCAGCATGTCAGAAAGCGAG 720
QY 1051 GCGAATTGCGCCAGCATCAGAAAGAA 1077
DB 721 GATGAATTCGCCAAACGCGAAGTAA 747

RESULT 10
US-08-750-145A-21
Sequence 21, Application US/08750145A
Patent No. 6010851
GENERAL INFORMATION:
APPLICANT: MIHARA, Yasuhiro
APPLICANT: UTAGAWA, Takashi
APPLICANT: YAMADA, Hideaki
APPLICANT: ASANO, Yasuhisa
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
TITLE OF INVENTION: Phosphate Ester
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08750,145A
APPLICATION NUMBER: US/08750,145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094690
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN P. CELON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
FEATURE:
NAME/KEY: CDS
LOCATION: 1..747
US-08-750-145A-21

Query Match 40.3%; Score 493.4; DB 3; Length 747;
Best Local Similarity 79.0%; Pred. No. 4.4e-154;
Matches 587; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
QY 331 ATGAAAAAGCGTCTGGCAGTTGTTTGGCGCATGTTCTCTCAGGCCCTGGCG 390
DB 1 ATGAAAAAGCGTCTGCTGCGCTTTGGCTTGGCGCATGTTCTCTCAGTTAGTGGCCTTTGGC 60
QY 391 CTGCTGCTACCGGCAACGACACTCACGAAACCGGATCTCTACTACCTCAAGAACAGT 450
DB 61 CTGCTTCCCGCGGCAATGATGCCACCACGAGCGGATCTCTACTCTGAAATGCC 120
QY 451 GAAGCCATTAAACAGCTTGGCGCTGTTTGGCGCATGTTTGGCGCATGTTTGGCGCATGTTTGG 510
DB 121 CAGGCCATTGACAGCTGCGGCTGTTTGGCGCATGTTTGGCGCATGTTTGGCGCATGTTTGG 180

QY 1051 GCCGAATTCGCCAGCATCAGAA 1073
DB 721 GACGAGTTTGGGAAACAGCAGAA 743

RESULT 12
US-09-417-090-25
Sequence 25, Application US/09417090
Patent No. 6355472
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
UTAGAWA, TAKASHI
YAMADA, HIDEAKI
ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,090
FILING DATE: 13-Oct-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE: 21-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
FEATURE:
NAME/KEY: CDS
LOCATION: 1..747
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-417-090-25

Query Match 40.3%; Score 493.4; DB 3; Length 747;
Best Local Similarity 79.0%; Pred No. 4.4e-154;
Matches 587; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 331 ATGAAAAACGTGTTCTGGCAGTTGTTTGGCGCAATGTTCTCTCTCAGGCCCTGGCG 390
DB 1 ATGAAAAAGCGTGACTCGCCCTTTGGCTTCCAGCCCTCTTTTTCAGTTAGCGCCCTTTCG 60

QY 391 CTGGTCGTACGGCAACGACACTACGACGAAACCGGATCTCTACTACTCTCAGGACAGT 450
DB 61 CTGGTTCCCGCGGCAATGATGCCACCAACCGACCGCATCTCTACTATCTGAAAAATGCC 120

QY 451 GAAGCCATTAAACAGCCTGGCGCTGTTGCCGCCACCAACCGCGGTGGCTCCATTGGCTTT 510
DB 121 CAGGCCATTGACAGCCTGGCGCTGTTGCCACCGCGCGGAACTGGGACAGCATTTGGCTTT 180

QY 511 CTCACGATCAGGCCATGATGAACAGGCGCGCTGCTGGCGCAACACCGACCGGTAAG 570
DB 181 TTAACAGATCAGCGCATGATGAGAAAGGCGCTGCTGGCGCGCACCGCGCGGCGAG 240

QY 571 CTGGCGCGGAAAGATGCAAACTGAGCAGTGGCGGGGTGGCGAATGCTTTCTCGGCGCG 630
DB 241 TTGGCGCGGAGATGCGACCTGAGCGCGGTGGCGGCGCAAGCGCTTCTCGCGCAGCA 300

QY 631 TTTGGTAGCCGATACCGGAAAAAGACGCCCCGGCGCTGCAATTAATTAATGACCAATATG 690
DB 301 TTGGCTCCCGGATCAGCGAAAAAGACGCCCCGGCGCTGCAAACTGCTCACCACATG 360

QY 691 ATTGAGAGCGCGGGGATCTGGCGACCGCGCAGCGGAAAGATCACTATATGCGCATTCGT 750
DB 361 ATTGAAGACCGCGGGGATCTGGCGACCGCGGCGGAGGAGGAGATATATGCGTATTCGT 420

QY 751 CCGTTCCGCTTTTATGGGCTCTCTACCTGTAAATACCAACGAGGACAACTCTTCCAAA 810
DB 421 CCGTTTGCCTTTACGCGGCTGTCACCTGCAATACCAACGAGGATAAGCTTCCGAAA 480

QY 811 AATGGCTCTTATCCGTCGGGCAATCTCTATCGGCTGGGCTACTCGCTGCTGCGCA 870
DB 481 AACGGCTCTTACCTTCCGACACACCTTATCGGCTGGGCGACCGCTGCTGCTGCGCC 540

QY 871 GAGATCAACCTCAGCGCCAGACGAGATCTTGAACCGCGGTTATGAGCTGGGCGCAGAGC 930
DB 541 GAAATCAACCCGACGCGCCAGATGAGATTTCTCAGCGCGGCTATGAGCTCGGTGAAAGT 600

QY 931 CGGCTGATTTGGGCTACCACTGSCAGATGATGATGATGATGATGATGATGATGATGAT 990
DB 601 CGGCTGATCTGGGCTTACCACTGSCAGATGATGATGATGATGATGATGATGATGATGAT 660

QY 991 GCCGTTGGGCGACCTGCGATACCAACCGCGGTTTCCAGCAGCAGCTTCCAGAAACCGAAG 1050
DB 661 GCGGTGGTTGCAACCTGCGATACCAATCGGCTTCCAGCAGCAGCTGCAAAACCGCAA 720

QY 1051 GCGGAATTCGCCAGCATCAGAA 1073
DB 721 GACGAGTTTGGGAAACAGCAGAA 743

RESULT 13
US-09-727-578-25
Sequence 25, Application US/09727578
Patent No. 6355472
GENERAL INFORMATION:
APPLICANT: MIHARA, YASUHIRO
APPLICANT: UTAGAWA, TAKASHI
APPLICANT: YAMADA, HIDEAKI
APPLICANT: ASANO, YASUHIISA
TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE
ESTER
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/727,578
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/975,698
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0885-0
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Klebsiella planticola
STRAIN: IFO 14939
NAME/KEY: CDS
LOCATION: 1..747
US-09-727-578-25

Query Match 40.3%; Score 493.4; DB 4; Length 747;
Best Local Similarity 79.0%; Pred. No. 4.4e-154;
Matches 587; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

331 ATGAAAACGCTGCTGGCAGTTGTTTGGCGCATGTTCTCTCTCAGGCCCTCGCG 390
1 ATGAAAAGCGTGACTCGCCCTTGCTTCCAGCCTCTTTCAGTTAGCGCCCTTGG 60
391 CTGCTGCTACCGGCAACGACACTACCAACGCGATCTCTACTACTCAAGAACAGT 450
61 CTGTTCCGCGGCAATGATGCCACCAAGCCGATCTCTACTATCTGAAAAATGCC 120
451 GAAGCAATTAAAGCCTGGCTGTGGCGGCAACACCGCGGCTGGCTCCATTCGGTT 510
121 CAGGCCATTGACAGCCTGGCTGTGGCGGCAACCGCGGCTGGCTCCATTCGGTT 180
511 CTCACGATCAGCCATGATGAACAGGCGGCTCTGCTGGCAACACCGAGCGGTAAG 570
181 TTAACGATCAGCGGATGATGAAGAGGCGCTCTGCTGGCGCAACCGCGCGCAAG 240
571 CTGCGCGGAGAGTSCAAACCTGAGCAGTGGCGGGTGGCGAATGCTTTCTCGCGCG 630
241 TTGGCGGAGAGATGCCAATCTGAGCGGGTGGCGTGGCGCAAGCCTCTCTCGCAGCA 300
631 TTGTAGCCGATCAGTGAAGAGAGCGCGCGGCTGCATAATTAATCTGACCAATAG 690
301 TTGCGCTCCCGATCAGCGAAAGAGCGCGCGGCTGCATAATCTGCTCCCAATAG 360
691 ATTGAGGAGCGCGGATCTGCGGACCGCGCGGCGGAAAGATCACTATATGCGCAATCGT 750
361 ATTGAAGAGCGGGGATCTGCGGACCGCGCGGCGGAAAGAGTATATGCGTATCTGT 420
751 CGGTTCCGGTTTATGGGCTCTACCTGTATATACACCGAGAGCAAACTGTCCAAA 810
421 CGGTTTGCCTTCTACGGCGTGTCCACTGCAATACCAAGAGAGTAAAGTGTGAAA 480
811 AATGGCTCTATTCGTCGGGATACCTCTATCGGCTGGGCTACTGCGCTGGTGGCA 870
481 AACGGCTCTTACCTTTCGGGACACACTCTATCGGCTGGGCGACCGCTGGTGGCC 540
871 GAGATCAACCTCAGCGCGAGAGATCTCTGAACGCGGTTATGAGCTGGGCGCAGAGC 930
541 GAAATCAACCGCGAGCGAGATGAGTTCTCAAGCGGCGCTATGAGCTCGTGAAGT 600
931 CGGCTGATTGGCGCTACCACTGCGAGAGTGTGGATGCCCGCGGGTAGTGGATCT 990

601 CGGCTGATCTCGGTTACCACTGCGAGCGCATGTTGACGCGCGCGGATGTTGCGCTCG 660
991 GCCGTTGTGGGACCCCTGCATACCAACCCGCGGCTTCCAGCAGCATTTCCAGAAAGCGAAG 1050
661 CGGCTGTTGCAACCTGCTGCATACCAATCCGCGCTTCCAGCAGCAGCTGCAAAAAGCCAAA 720
1051 GCCGAATTCGCCAGCATCAGAA 1073
721 GACGAGTTTGGAAACACAGAGAA 743

RESULT 14
US-08-750-145A-2
Sequence 2, Application US/08750145A
Patent No. 6010851
GENERAL INFORMATION:
APPLICANT: MIHARA, Yasuhiro
APPLICANT: UTAGAWA, Takashi
APPLICANT: YAMADA, Hideaki
APPLICANT: ASANO, Yasuhisa
TITLE OF INVENTION: Method for Producing Nucleoside-5'-
TITLE OF INVENTION: Phosphate Ester
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFF. DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,145A
FILING DATE: 01-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-149781
FILING DATE: 05-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-094680
FILING DATE: 26-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0010-0830-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 750 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Morganella morganii
STRAIN: NCIMB 10466
FEATURE:
NAME/KEY: CDS
LOCATION: 1..747
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..50
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 61..747

US-08-758-145A-2

Query Match 34.4%; Score 422; DB 3; Length 750;
Best Local Similarity 72.7%; Pred. No. 2.8e-130;
Matches 545; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 331 ATGAAAGAGTGTCTGCGAGTTGTTTGGCGGATGTTCTCTCAGGCGCTGGCG 390
DB 1 AAGAAAGAGTATTATCGCGGTGTTCTCTCTACTGTTTCCCTTCCGCGCTGGCC 60

QY 391 CTGGTCGTACCGGCAACGACATACACGAAACCGGATCTCTACTACCTCAAGAACAGT 450
DB 61 GCGATCCGCGGCGCAACGATGCGACCAAGCGGATTTATATTATCTGAAAAATGAA 120

QY 451 GAAGCCATTAAACGCTTGGGCTGTTGGCGGCAACCGCGGCTGGCTCCCTGGTTT 510
DB 121 CAGGCTATCGACAGCTGAACTGTACCGCCACCGCGGAGTGGCAGATTTCAGTTT 180

QY 511 CTCAGGATCAGGCGGATGATGAACAGGCGGCTGCTGCGCAACCGGATCTCTACTACCTCAAGAACAGT 570
DB 181 TTAAATGATCAGGCAATGATGAGAAAGGCGGCTGCTGCGCAATACCGAGCGCGGAAA 240

QY 571 CTGGCGCGGAAAGATGCAAACTCTGAGCAGTGGCGGCTGGCGAATGCTTTCTCGCGCGCG 630
DB 241 CAGGACAGGAGATGCTGACCTGGCGCGAGGGGTGGCAACCGCAATTTTCAGGGGCA 300

QY 631 TTGGTAGCGGATCAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
DB 301 TTGGTAGCGGATCAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360

QY 691 ATGAGGAGCGCGGAGTCTGGGACCGCGGAGCGGAAAGATCACTATATGCGCATTCGT 750
DB 361 ATTGAGATGCGGATGATCTGTCACCGCTGCGGAGAGAGAGAGAGAGAGAGAGAG 420

QY 751 CCGTTCCGTTTATGGGGTCTCTACTGTAAATACACCGGAGAGAGAGAGAGAGAGAGAG 810
DB 421 CCGTTCCGTTTATGGGGTCTCTACTGTAAATACACCGGAGAGAGAGAGAGAGAGAGAG 480

QY 811 ATGGCTCTTATCGTCCGCGGATACCTCTGCTGGGCTGCTGCTGGCTGGTCTGGCA 870
DB 481 AACGGATCTTACCGCTGAGTCTATCTGCTGGGCAACCGGAGTGGTGGCG 540

QY 871 GAGATCAACCTCAGCGCCAGAGAGAGATCTGAAACCGGTTATGAGCTGGGCGAGAGC 930
DB 541 GAAGTGAACCGGCAATCAGGATGCGATCTGGAACGGGTTATCAGCTCGGACAGAGC 600

QY 931 CGGCGATTTGGGCTACCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 990
DB 601 CGGCGATTTGGGCTACCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660

QY 991 GCGGTTGGGCGGCTGATACCAACCGCGGTTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 1050
DB 661 GCGGCTGCGGAGATTACATTCGATTCGCGGATTCAGGCGGAGTTAGGAAAGCGCAA 720

QY 1051 GCGGAATTCGCGGAGCTGAGAAATAA 1080
DB 721 CAGGAATTCGCAAAATCAGAGAAATAA 750

RESULT 15

US-08-975-698A-2

Sequence 2, Application US/08975698A

Patent No. 6015697

GENERAL INFORMATION:

APPLICANT: MIHARA, YASUHIRO

APPLICANT: UTAGAWA, TAKASHI

APPLICANT: YAMADA, HIDEAKI

APPLICANT: ASANO, YASUHIKA

TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEOSIDE-5'-PHOSPHATE

TITLE OF INVENTION: ESTER

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/975,698A

FILING DATE: 21-NOV-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 0010-0885-0

TELEPHONE: (703) 413-3000

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INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 750 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Morganella morganii

STRAIN: NCIMB 10466

FEATURE:

NAME/KEY: CDS

LOCATION: 1..747

FEATURE:

NAME/KEY: sig_peptide

LOCATION: 1..60

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 61..747

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QY 391 CTGGTCGTACCGGCAACGACATACACGAAACCGGATCTCTACTACCTCAAGAACAGT 450
DB 61 GCGATCCGCGGCGCAACGATGCGACCAAGCGGATTTATATTATCTGAAAAATGAA 120

QY 451 GAAGCCATTAAACGCTTGGGCTGTTGGCGGCAACCGCGGCTGGCTCCCTGGTTT 510
DB 121 CAGGCTATCGACAGCTGAAACTGTATACCGCCACCGCGGAGTGGCAGATTTCAGTTT 180

QY 511 CTCAGGATCAGGCGGATGATGAACAGGCGGCTGCTGCGCAACCGGATCTCTACTACCTCAAGAACAGT 570
DB 181 TTAAATGATCAGGCAATGATGAGAAAGGCGGCTGCTGCGCAATACCGAGCGCGGAAA 240

QY 571 CTGGCGCGGAAAGATGCAAACTCTGAGCAGTGGCGGCTGGCGAATGCTTTCTCGCGCGCG 630
DB 241 CAGGACAGGAGATGCTGACCTGGCGCGAGGGGTGGCAACCGCAATTTTCAGGGGCA 300

QY 631 TTGGTAGCGGATCAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
DB 301 TTGGTAGCGGATCAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360

QY 691 ATTGAGGAGCGCGGAGTCTGCGGAGCGGCGGAAAGATCACTATATGCGCATTCGT 750

